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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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                 Published Applications AA: *
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// Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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// Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
// Cgn2_6/ptodata
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US-09-877-156-20

US-09-877-156-20

US-09-877-156-2

US-09-062-113-71

US-09-062-113-75

US-09-062-113-75

US-09-062-113-75

US-09-062-113-74

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US-09-894-924-1
US-09-935-727-2
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Compugen Ltd.
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W	N -	2	е 6,	Sequence 17, Appl	e 17	17		Sequence 3, Appli	e 67,	Sequence 20, Appl	, 0	9	e 76,	e 11,	e 81,	e 63,	e 2,	e 1,	(D	e 66,	e 65,	equence 64,	(D (5	e 7	Sequence 79, Appl

ALIGNMENTS

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APPLICANT: ASKRENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: TITI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUWAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DGR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 06/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1998-07-30
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SEQ ID NO 1
LENGTH: 300
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Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
                                                                               VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
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100.0%; Pr
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Pred. No. 8.8e-107;
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR PILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-11-21
PRIOR PILING DATE: 2000-11-21
PRIOR PELING DATE: 2000-08-25
PRIOR PELING DATE: 2000-08-25
PRIOR PELING DATE: 2000-08-25
PRIOR PELING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 1999-08-03
PRIOR PLING DATE: 1999-08-03
PRIOR PLING DATE: 1999-08-03
PRIOR PELING DATE: 1999-04-20
PRIOR PELING DATE: 1999-04-27
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PRIOR PELING DATE: 1999-04-27
PRIOR PELING DATE: 1999-03-04
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PRIOR PELING DATE: 1999-03-14
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: 60/124,095
PRIOR PELING DATE: 1999-03-18
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PRIOR PELING DATE: 1999-03-18
PRIOR PELING DATE: 1999-03-18
PRIOR PELING DATE: 1999-03-19
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               Sequence 2, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
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Matches 271; Conservative
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SEQ ID NO 2
LENGTH: 300
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                                            COPCPPGTFSASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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APPLICANT: DOUGE, KELLY H.
APPLICANT: DONGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
ITILE OF INVENTION: DCR3 POLYDEDCIGG, A TNFR HOMOLOG
FILE REFERENCE: PI134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1998-07-30
SRIOR PILING DATE: 1998-07-30
NUMBER: OF SEQ ID NOS: 18
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Pred. No. 8.8e-107;
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US-09-894-924-1
; Sequence 1, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
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US-09-894-924-1
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Best Local Similarity
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Matches 271;
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61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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   Length 300;
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100.0%; Score 1491; DB 10;
100.0%; Pred. No. 8.8e-107;
ive 0; Mismatches 0;
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209

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Gaps

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; FEATURE:
, NAME/KBY: misc feature
; LOCATION: (79)
; OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2
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US-09-840-795-2
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; ORGANISM: Homo sapien
US-09-877-156-17
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/351,777
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 300
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Murphy, Erin E.
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Best Local Similarity
Matches 270; Conserv
                                                                  Query Match
Best Local Similarity
Matches 268; Conserv
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CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
                                                                                                                                                                                                                        ORGANISM: primate
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                    VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPMTCGPCPPRHYTQFWNYLERCR
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llarity 98.9%;
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Pred. No. 1.1e.
0; Mismatches
                                                                  Score 1469; DB 10;
Pred. No. 4.2e-105;
0; Mismatches 3;
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.1e-105;
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CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
                                                                                                                                                                    Sequence 2, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
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Patent No. US20020055625A1
GENERAL INFORMATION:
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Best Local
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND THER FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR PELING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 113
                                                90 YCNVLCGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 142
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APPLICATION NUMBER: US/09/062,113
FLING DATE: 17-APR-1998
CLASSIFICATION NUMBER: US/09/062,113
FLING DATE: 17-APR-1998
CLASSIFICATION NUMBER: US/09/062,113
APPLICATION NUMBER: US/09/062,113
APPLICATION NUMBER: US/09/062,1195
FILING DATE: 20-FEB-1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, RONG P.
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
NAME: MOORE, RONG P.
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
NAME: MOORE, RONG P.
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
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LOCATION: 1..305
OTHER INFORMATION: /note= "OCIF-DDD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             ; Sequence 71, Application US/09062113; Patent No. US20020051969A1; GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS:
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MEDIUM TYPE: Floppy
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CITY: Boston
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US-09-062-113-71
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US-09-935-727-4
US-09-935-727-4
US-09-935-727-4
US-08-20201505633A1
GENERAL INFORMATION:
FAPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REPERENCE: FP45-42
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT APPLICATION NUMBER: US/03/324
FRIOR APPLICATION NUMBER: 60/252,131
FRIOR APPLICATION NUMBER: 60/252,131
FRIOR PILING DATE: 2000-10-70-6
FRIOR PILING DATE: 2000-10-70-6
FRIOR PILING DATE: 2000-08-25
FRIOR PILING DATE: 2000-08-25
FRIOR PILING DATE: 1999-12-01
FRIOR APPLICATION NUMBER: 60/146,371
FRIOR APPLICATION NUMBER: 60/146,371
FRIOR PILING DATE: 1999-04-27
FRIOR PILING DATE: 1999-04-27
FRIOR PILING DATE: 1999-04-27
FRIOR PILING DATE: 1999-04-27
FRIOR PILING DATE: 1999-03-04
FRIOR APPLICATION NUMBER: 60/131,270
FRIOR PILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120
                                                                                                                                                                                                                                                                                       56 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                         116 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 175
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                                                                                                                                                                                                                                 °,
                                                                                                                                                                  56.4%; Score 841; DB 10; Length 153; 100.0%; Pred. No. 1.4e-57; cive 0; Mismatches 0; Indels
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US-09-935-727-4
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 153; Conserv
SEQ ID NO 2
LENGTH: 153
TYPE: PRT
ORGANISM: human
                                                                                                                  US-09-877-156-2
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Patent No. US20020051969A1
                                                                APPLICATION NUMBER: JP 549
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JI
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JI
APPLICATION SOFEB-1996
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APPLICANT: HIGASHIO, Kamji
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS: ADDRESSE: Testa. Havener.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/062,113 FILING DATE: 17-APR-1998 CLASSIFICATION:
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125 High St.
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SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
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                                                                         MBER: PCT/JP96/00374
20-FEB-1996
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US 08/915,004
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US-09-062-113-75
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Best Local Similarity 41.2%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acid
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              APPLICANT:
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     APPLICANT:
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                                                                                                                        CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 EEAFFRF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 ERAVIDF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 LCGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPFGAGVIAFGTFSQNTQCQPC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 44
REFERENCE/DOCKET NUMBER:
                                                                                             STREET:
                                                                                                            ADDRESSEE:
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OTHER INFORMATION:
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                                               COUNTRY:
                                                                            CITY: Boston
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US20020051969A1
                                      MA
USA
                                                                                             E: Testa, Hu
125 High St.
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YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
                                                                                                                                                                                     HIGASHIO,
                                                                                                                                                                                                                                                                                                           TSUDA, Eisuke
MOCHIZUKI, Shin'ichi
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                                                                                                                                                                                                                                                                           KOBAYASHI, Fumie
                                                                                                                                                                                                                                                                                                                                          GOTO, Masaaki
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the Proteins
                                                                                                            Hurwitz & Thibeault
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86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145
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APPLICANT: TUNAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
ITILE OF INVENTION: DCR3 POLYPEPTIGE, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 293
                                                                                                                                                              TITLE OF INVENTION: DCR3 POLYPEDTIDE, A TNFR Homolog FILE REFERENCE: P1134R2 REVISED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
29.5%; Score 440.5; DB:
Best Local Similarity 41.2%; Pred. No. 9.2e-27
Matches 77; Conservative 31; Mismatches 74
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
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GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
                            PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.
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ROY, MARGARET A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-896-096A-18
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ORGANISM: Homo sapiens
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US-09-894-924-18
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APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LUCATION: 1..251
; OTHER INFORMATION: /note= "OCIF-CDD2"
US-09-062-113-75
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTONNEY/AGENT INFORMATION:
NAME: MOORE, ROING P.
REGISTRATION NUMBER: FJN-060DV
TELECOMUNICATION INFORMATION:
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Perent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKENNZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN, L.
APPLICANT: GIRNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
                                                                                                                              UMBER: US/09/062,113
17-APR-1998
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TYPE: amino acid
STRANDEDNESS:
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FEATURE:
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide LOCATION: -21..0
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                                                                                                                                                                         FILING DATE: 17 CLASSIFICATION:
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RESULT 14
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                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                  COMPULEA.

OPERATING SYSTEM: PC-DOS/MS-LUC

SOFTWARE: PatentIn Release #1.0, V
SOFTWARE: PATENTION DATA:

CURRENT APPLICATION DATA:

US/09/062,113
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: JPC-DOS/MS-DOS

COMPATING SYSTEM: PC-DOS/MS-DOS
                                                APPLICATION NUMBER: PCT/JP96/0037
FILING DATE: 20-PEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing TITLE OF INVENTION: the Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: L. Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                              TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 17-APF
                                                                                                                                                                                                                                                                            CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERAVIDE 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Testa, Hu
125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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HIGASHIO, Kanji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
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SHIMA, No. US20020051969Aluyuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
                                                                                                                                                                                 JP 207508/1995
                                                                                                                         PCT/JP96/00374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 440.5; DB 10; Pred. No. 9.2e-27;
                                                                                                                                                                                                                                                                                                                                                  Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72,
Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 248-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: Protein
LOCATION: 1..300
OTHER INFORMATION:
                                                                                                                                                                                                                       APPLICANT: HIGASHO, Kanji
TITLE OF INVENTION: No. US20020051969Alel Proteins
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                     COUNTRY: US
ZIP: 02110
                                                                                                                                       CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEAFFRF 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09062113
                                                                                                                                                                       125 High St.
                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : (617) 248-7000
(617) 248-7100
                                                                                                                                                                                                                                                                                                                                             KOBAYASHI, Fumie
SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
                                                                                                                                                                                                                                                                                                           NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
                                                                                                                                                                                                                                                                                                                                                                                                                 MOCHIZUKI, Shin'ichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO, Masaaki
                                                                                                                                                                                                                                                                                                                                                                                                 Kazuki
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eisuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%; Score 440.5; DB 41.2%; Pred. No. 1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "OCIF-CSph"
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                   Version
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                                                                                                                                                                                                                                                             and Methods
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                                                                                                                                                                                                                                                         for Producing
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APPLICATION NUMBER: US/09/062,113
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: UP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION NUMBER: UP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION NUMBER: PCT/JP96/00374
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
FILING APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGAT INFORMATION:
NAME: MOOSE, RONG APPLICATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FUN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: GHARACTERISTICS:
LENGTH: 327 amino acids
TYPOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: PEPLICATION
PRANTKEY: PEPLICATION
PROTECTION
PROTECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: 1.306 OTHER INFORMATION: /note= "OCIF-DDD2"
US-09-062-113-72
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;; ;; 26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLXCSP 85 5; Gaps 5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64 Query Match

29.5%; Score 440.5; DB 10; Length 327;
Best Local Similarity 41.2%; Pred. No. 1e-26;
Matches 77; Conservative 31; Mismatches 74; Indels 5; ò

g

65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124 g ò

125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182 ò

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183 ERAVIDF 189 ò

203 EEAFFRF 209

Search completed: January 6, 2003, 11:27:02 Job time : 37 secs

5.1.3

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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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length: 2000000000
A Geneseq 101002:*

1: \SID52\gcgdata\geneseq\geneseq\-emb1\AA1980.DAT:*
2: \SID52\gcgdata\geneseq\geneseq\-emb1\AA1981.DAT:*
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23: \SID52\gcgdata\geneseq\geneseq\geneseq\-emb1\AA1993.DAT:*
                   January 6, 2003, 11:15:31 ; Search time 61 Seconds (without alignments) 591.982 Million cell updates/sec
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and is score Pred. No. No. is the number of results predicted by chance greater than or equal to the score of the result derived by analysis of the total score distribution to have being pr printed,

SUMMARIES

10	9	8	7	σ	5	4	ω	N	1	Result No.
1491	1491	1491	1491	1491	1491	1491	1491	1491	1491	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
271	271	271	271	271	271	271	271	271	271	Query Match Length DB
23	22	22	22	22	21	21	21	21	20	BB
AAE14578	AAB74465	AAB68047	AAB68044	AAE03567	AAY96598	AAY97247	AAB19705	AAB19334	AAY42184	ID
Human mature FLINT	Human FLINT mature	Amino acid sequenc	Amino acid sequenc	Human mature fas 1	Human mature FLINT	M68 TNF receptor r	Human FAS ligand i	A mature human FAS	Human mFLINT #1 pr	Description

ALIGNMENTS

RESULT 1

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30-MAR-1998;
20-MAY-1998;
09-SEP-1998;
17-DEC-1998;
18-DEC-1998;
18-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                        Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL; apoptosis; inflammation; cancer; diabetes, acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia, differentiation; growth; myelodysplastic syndrome; pancytopenic condition; myocardial ischaemia.
                                                                                                                                                                                                                                                                      Human mFLINT #1 protein sequence.
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                                                                                                                                                                    Homo sapiens
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                   98US-0079856.
98US-0086074.
98US-0099643.
98US-0112577.
98US-0112577.
98US-0112703.
98US-0112933.
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chronic obstructive pulmonary disease; Crohn's disease.
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                           Homo sapiens
The present invention describes therapeutic applications of mature FilnT (mFilNT) for use in the treatment of acute liver failure. Mature FilnT (mFilNT), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated correndolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage or damage to an confiscant bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that chave been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
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                                                                                                                        Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
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                        Hale JE, Heuer JG;
Noblitt TW, Reidy CA;
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                        Bumol TF, Dou S, Glasebrook AL, Gould KE,
Hui KY, Kharitonenkov A, Mizrahi J, Na S,
Song HY, Wang J, Wu X, Zuckerman SH;
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Matches 271; Conservative
(ELIL ) LILLY & CO ELI.
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with

"optionally replaced with Thr" "optionally replaced with Leu"

"optionally replaced with Tyr"

Glu or Thr"

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"optionally replaced with Asn"

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Matches 271
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21-JUN-1999;
21-JUN-1999;
20-OCT-1999;
                                                                                                                   The present sequence represents a mature human FAS Ligand Inhibitory Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
                                                                                                                                                                                                                                                                                                                                                                   Becker GW,
Newton CM,
                                                                                                                                                                                                                                                                            FAS Ligand Inhibitory Protein analogs useful for treating abnormal apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease ulcerative colitis or Crohn's
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VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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271; Conserv
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                                                                                        271 AA
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99US-0140077.
99US-0140156.
99US-0160566.
2000US-0183398.
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Mismatches 0;
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                                                                                                                                  "optionally replaced by any naturally occurring amino acid, preferably Tyr given in Claim 9"
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                                                                                                                                                                                                                                                                                                                                                   "optionally replaced occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                "optionally replaced Claims 11 and 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "optionally replaced Claims 11 and 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "optionally replaced by Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cleaved by trypsin-like proteases"
                                                                                            "optionally replaced
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            "optionally replaced by any naturally occurring amino acid, preferably Gln, Glu, Ala, Gly, Ser, Val, Tyr or Asn as given in Claims, 9, 10, 11, 12, especially Gln as given in Claims 13, 14, 15, 35 and 36"
                                                                                                                                                                                                                occurring amino
given in Claims
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99US-0172754.
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20-DEC-1999;
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AAY97247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of human FAS ligand inhibitory protein FLINT mature protein. FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with homologue that binds FAS ligand, preventing its interaction with lands and the second of the secon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel protease resistant FAS ligand inhibitory protein analogues resistant to in vivo or in vitro proteolysis at amino acid position 218 of the mature protein, useful for treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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/note= "optionally replaced by any naturally occurring amino acid"
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/note= "optionally replaced by occurring amino acid"
                                                                 /note= "optionally replaced by occurring amino acid"
                                                                                                       Misc-difference 221 /note= "optionally replaced by
                                                                                                                                                      occurring amino acid"
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99US-0140073.
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Best Local Similarity
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N-PSDB; AAA88730
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04-AUG-1999
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The M68 protein is a member of a family of proteins which have roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis-related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying conditions diseases associated with abnormal levels of
121 CQPCPPGTFSASSSSSSCQQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                                                             240
                                                                                M68; tumour necrosis factor; TNF; programmed cell death; apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemate lupus erythematosus; Hashimoto's thyroiditis; Carave's disease; idiopathic myxodema; autoimmune diabetes; thrombotic thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcarative colitis; glomerulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemis; myelodisplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteopozosis, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                       M68 TNF receptor related protein (mature protein)
                                                                                                                                                                                   271
                                                                                                                                            GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                      FILINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR; FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anamic; neuroprotective; anti-ulcer; cytostatic; anti-inflammatory; antibacterial; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxodema, autoimmune diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis, liver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephritis, pulmonary fibrosis, heart failure, atherosclerosis, aplastic anaemia, myelodisplastic syndromes, osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
transplantation
         Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ
                                                                                                                                                                                                                                                      WO200037094-A2
                                                    N-PSDB; AAA51077.
                                                                                                                                              20-OCT-1999;
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30-MAR-1999;
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                                                                                          Posada JA,
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                                                                                                                                                                                                                                                                                                                                                                                                    (first
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                                                                                                                                            98US-0113407.
99WO-US06797.
99US-0172239.
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Best Local Similarity
Matches 271; Conserv
                                                                                                                           Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TWFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS; acute respiratory distress syndrome; pulmonary fibrosis; pP; therapy; chronic obstructive pulmonary disease; COPD; acute lung injury; goitre; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis; fibroric lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diabetes mellitus (IDM); inflammatory bowel disease; crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; chown's syndrome; multiple sclerosis; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating acute respiratory distress syndrome, treating or inhibiting ulcerative colitis, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation mFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepaticis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                04-AUG-2001
                                                                               Homo
                                                                                                                   neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE03567 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Fig 3; 125pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQPCPBGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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                                                                                                                                                                                                                                                                                                                                                                     mature fas ligand inhibitory protein (FLINT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLINT (also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1491; DB 21; ilarity 100.0%; Pred. No. 8.5e-115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          so known as osteoprotegrin 3) is a new tumour necrosis (TNFR) superfamily member, which binds FasL and LIGHT and
                                  Location/Qualifiers
  /note=
                                                                                                                   vasotropic.
"N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271
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The present sequence is human mature fas ligand inhibitory protein

(FILNT). FLINT, a homologue of tumour necrosis factor receptor

(FILNT). FLINT, binds fas ligand (FasL) and thereby preventing the

protein (TNFR) binds fas ligand (FasL) and thereby preventing the

construction of FasL with fas. FLINT comprising O-linked or N-linked

oligosaccharides is useful for preventing or treating acute lung injury

(ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,

chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PP),

conficiente organ preservation for transplantation and to inhibit T

conficient as rheumatoid arthritis, fibroproliferative lung disease,

fibrocic lung disease, acute lung injury, human immunodeficiency virus

(HIV), ischaemia, brain trauma/Anjury, chronic renal failure, graft-ve-

host disease, cutaneous inflammation, vascular leak syndrome,

CHelicobacter pylori infection, goitre, atherosoflerosis, insulin dependent

diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,

Crohn's disease, sepais, pancreatitis, cancer, autoimmune disease such as

Crohn's disease, sepais, pancreatitis, cancer, autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECERAVIDEVAFODISIKRLORLLOALEAPEGWGPTPRAGRAALQLKLKRRLTELLGAQD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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                                             /incte= "O-linked glycosylation site"
218..219
/note= "Proteolytic cleavage"
               'note= "O-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 52-53; 60pp; English.
                                                                                                                                                                                                                                           99US-0169367.
99US-0169381.
99US-0169412.
                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191430
                                                                                                                                                                                                       29-NOV-2000; 2000WO-US30166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                         (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                     2001-381684/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligosaccharides -
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                                                                                                                                                                                                                                                                                                                                                                                 Witcher DR;
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                                                                                                                                WO200142463-A1
Modified-site
                                   Modified-site
                                                                         Cleavage-site
                                                                                                                                                                                                                                                 07-DEC-1999;
                                                                                                                                                                                                                                                              07-DEC-1999;
07-DEC-1999;
                                                                                                                                                                     14-JUN-2001
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The present sequence represents a mature FLINT (FAS Ligand Inhibitory Protein) polypeptide. The specification describers a composition comprising a divalent metal cation and FLINT protein. The composition is used either for reducing, reversing or eliminating aggregation and precipitation of FLINT or for inducing oligomerisation or aggregation of FLINT molecules. They can be used for purifying FLINT and/or maintaining FLINT in solution. The compositions are used to treat and/or prevent disorders associated with the binding of Fas to Fast and/or LIGHT to the LTbetaR and/or FRZ/HVEM receptors. Uses include the treatment of acute liver failure and cerebral ischemia and the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCNVI.CGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions comprising a divalent metal cation and a FAS Ligand Inhibitory Protein (FLINT), for reducing or inducing aggregation of FLINT and for treating diseases involving FasL/Fas and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPCPPGTFSASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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                                                                                                                                                                                                                           Fas;
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                                                                                                                                                                                                                       FLINT, FAS ligand inhibitory protein; divalent metal cation, Fe
Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                             Amino acid sequence of a human mature FLINT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1491; DB 22; 100.0%; Pred. No. 8.5e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGHT/LT-beta-R receptor interactions
Example 1; Page 39-40; 44pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                              Protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Witcher
                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2000; 2000WO-US20807.
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0153339
                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tian Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-273382/28.
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                                                                                                                                                                                                                                                                                                         WO200118055-A1.
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                                                                                                                              AAB68044;
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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human mature FLINT (FAS Ligand Inhibitory Protein) polypeptide. The specification describers a composition comprising a divalent metal cation and FLINT protein. The composition is used either for reducing, reversing or eliminating aggregation and precipitation of FLINT or for inducing oligomerisation or aggregation of FLINT molecules. They can be used for purifying FLINT and/or maintaining FLINT in solution. The compositions are used to treat and/or prevent disorders associated with the binding of Fas to FasL and/or LIGHT to the LTDetaR and/or TR2/HVEM receptors. Uses include the treatment of acute liver failure and cerebral ischemia and the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions comprising a divalent metal cation and a FAS Ligand Inhibitory Protein (FLINT), for reducing or inducing aggregation FLINT and for treating diseases involving FasL/Fas and/or LIGHT/LT-beta-R receptor interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 30-31; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-273381/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-2000; 2000WO-US20805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-2001
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                                                                                         CQPCPPGTF$ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                         VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
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                                                     CQPCPPGTF$ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
                                                                                                                                                                    YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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Pred. No. 8.5e-115;
0; Mismatches 0;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a composition comprising a divalent metal cation associated with a protease resistant Fas ligand inhibitory protein (FLINT) analogue. The composition is useful in the treatment of diseases associated with Fas binding to its ligand, such as acute liver failure, inflammatory diseases, cerebral ischaemia and apoptosis. The present sequence is the mature FLINT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 41-42; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions useful for reducing/inducing aggregation of a FLINT anacomprise a divalent metal cation and a protease-resistant FAS Ligand Inhibitory Protein (FLINT) analog -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human FLINT mature protein.
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                                 ECERAVIDEVAFQDISIKRIQRILIQALEAPEGWGPTPRAGRAALQIKIRRRITEILIGAQD 240
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                                                                                                                                                                                                           YCNVLCGERBEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Pred. No. 8.5e-115;
; Mismatches 0;
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This is the amino acid sequence of the human tumour necrosis related receptor (TR4), used in the method of the invention. The TR4 protein or its agonist can be used to treat a subject in need of enhanced TR4 polypeptide activity. The antagonist is used to inhibit TR4 polypeptide activity. The active agents can be used for the treatment and prevention of diseases such as chronic and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation, arthritis, septicaemia, autoimmune diseases, transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding tumour necrosis related receptor - used to treat vent e.g. inflammation, arthritis, septicaemia, autoimmune 3, transplant rejection, infection, stroke, ischaemia, ARDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, tumour necrosis related receptor; TR4; agonist, antagonist, inhibition, chronic; acute; inflammation; arthritis; septicaemia; autoimmune disease; transplant rejection; stroke; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VAETPIYFWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
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CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
                                                                                           ECERAVIDEVAFQDISIKRLORLLOALBAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of tumour necrosis related receptor (TR4)
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                                                                                                                                                                                                                                                                                                                AAW66102 standard; Protein; 300
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AA;
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AAW66102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new method of administering FLINT (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory diserses syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS)). The method minimises the pain and disconfort of injection methods. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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                                                                                                                                                                                                                                                                                                              FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis; organ failure; liver; kidney; panoreas; inflammatory disease; neutrophil; sepsis, acute respiratory distress syndrome; acute lung injury; systemic inflammatory response syndrome; sIRS; multiple organ dysfunction; MODS; human.
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    241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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                                                                                                                                           standard; Protein; 271
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                                                                                                                                                                                                                                                                              Human mature FLINT protein.
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Matches 271; Conservative
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N-PSDB; AAD27868.
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                                                                       The present sequence represents the human tumour necrosis factor receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides for the TNFR-6 beta protein (AAW63023). TNFR-6 alpha and TNFR-6 beta are members of the tumour necrosis factor receptor (TNFR) family. TNFRs are expressed in endothelial cells, keratinocytes, normal prostate and prostate tumour tissue. For a number of disorders of these cells, particularly of the immune system, substantially altered (whether increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR 6 alpha and TNFR-6 beta genes can also be detected. The TNFR beta polypeptides are also claimed to be useful for identifying ligands which may be useful to be useful for identifying ligands which may be useful
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Fig 1; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor receptors the diagnosis of immune system-related
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DB; AAV39085.
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                                                     apoptosis related disorders
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Sequence

This invention describes a novel tumour necrosis factor (TNF) receptor (I) isolated from human lung tissue. (I) is used: (i) to raise specific antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands

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ARESULT 13
AAY03099
ID AAY030
XX AAY03
AC AAY04

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Best Local Similarity
Matches 271; Conserv
                                                                                                  Claim 1;
                                                                                                                                                                             New soluble member of tumor necrosis factor receptor family, useful for identification specific modulators and for treating disease e.g. tumors
                                                                                                                                                                                                                                                          N-PSDB; AAZ09998
                                                                                                                                                                                                                                                                                                                                Kroeger B;
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                                                                                                  Page 8-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rosis factor; TNF; TNF receptor; human; lung; gene therapy; immunoassay; diagnosis; disease; immune system; tumour; system; cardiovascular system; central nervous system; asthma; nervous systems; transplant incompatibility; antitumor; arthritis; antiasthmatic; antiarthritic.
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/product= "TNF-receptor"
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Pred. No. 9.6e-115;
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expressed from a gene therapy vector) in conditions associated with a deficit of (1). Ab are used: (a) for qualitative or quantitative or deficit of (1). Ab are used: (a) for qualitative or quantitative or cacetion of (1) in standard immunoassays (for diagnosis of disease, or susceptibility, or for monitoring); and (b) as therapeutic inhibitors in cases where (1) is overexpressed. Nucleic acid (11) that encodes (1) is used: (A) for recombinant production of (1); (B) also its oligonucleotide fragments, in standard hybridization and/or amplification assays; (C) as source of antisense molecules or ribozymes; and (D) to produce transgenic animals (for studying (patho) physiology of (1)). Diseases possibly associated with under- or over-expression of (1) are those of the immune, osteogenic, cardiovascular and central or peripheral nervous systems, transplant incompatibility, asthma and rheumatoid arthritis. The products of the invention have antitumnor, antiasthmatic and antiarthritic activity. This sequence represents the TNF-receptor of the
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myocardial ischaemia.
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100.0%; Pred. No. 9.6e-115;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         300 AA;
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09-SEP-1998;
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The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor (mFLINT), which is a member of the tumour necrosis factor receptor the liver, abnormal hepatocyte apoptosis, adisorder associated with inflammation, hepaticis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage or damage to an classification tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating heematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
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Noblitt TW, Reidy CA;
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                                                                                                                                                                                          Dou S, Glasebrook AL, Gould KE,
Kharitonenkov A, Mizrahi J, Na S,
Wang J, Wu X, Zuckerman SH;
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98US-0112703.
98US-0112933.
98US-0113407.
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N-PSDB; AAZ25375.
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Song HY, Wang J,
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22-DEC-1998;
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Matches 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a mammalian tumour necrosis factor receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis factor receptor family, and can be used: (i) to raise specific antibodies (Ab), (ii) to treat osteopenic disorders associated with excessive osteoclast activity, e.g. primary osteopyroic metastases; (iii) for affinity purification of malignancy, or osteolyric metastases; (iii) for affinity purification of cognate ligands, and (iv) to screen for ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents such as soluble forms of the protein, are used to prevent, or reduce severity of, an immune response, and for treating cancer. They can also be used in diagnostic assays. The nucleic acid sequence encoding OPG-2 can be used as a probe to isolate related sequences from other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 18; 22pp; English.
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N-PSDB; AAX76052.
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24-NOV-1997;
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US-08-974-186-6
US-08-975-447A-6
US-08-975-446B-6
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US-08-974-186-6
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Sequence 127, Appli
Sequence 128, Appli
Sequence 14, Appli
Sequence 4, Appli
Sequence 20, Appli
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                                                                              ; MOLECULE TYPE: US-08-794-796-2
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US-08-794-796-2
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Patent No.
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corporatio
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
EILING DATE: US/08/794,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Emery,
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
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APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis
TITLE OF INVENTION: TR4
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acid
TYPE: amino acid
STRANDEDESS: single
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CORRESPONDENCE ADDRESS
                                                                                                                            TOPOLOGY:
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    Application US/08794796
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Tan, KB
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US-08-706-945D-130
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US-09-006-353A-4
US-09-006-353A-4
US-09-573-986-4
US-08-477-398-2
US-08-477-347-3
US-08-4776-862-2
US-08-974-022-48
US-08-795-445A-48
US-08-795-445B-48
US-08-795-446B-48
US-08-795-446B-48
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         Score 1491; DB 2
Pred. No. 3e-124;
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Query Match 100.

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APPLICANT: Boyle, Willaim J.
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; ORGANISM: human
US-09-286-529-2
                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo
US-09-286-529-20
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US-09-286-529-2
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                                                        30 VAETPIYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTGGPCPPRHYTQFWNYLBRCR 89
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Gaps
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Indels
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Patent No. 6297367
GENERAL INFORMATION:
APPLICANT:
Catherinon: New MEMBERS OF THE AND THER FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
GENERAL TAILORY: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF THE AND THER FAMILIES
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99.0%; Score 1476.5; DB 4.
Best Local Similarity 99.6%; Pred. No. 5.7e-123;
Matches 270; Conservative 0; Mismatches 0;
Mismatches
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Conservative
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LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapien
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US-09-286-529-17
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Matches 271;
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TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REPERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                     Score 1034; DB 4;
Pred. No. 4.8e-84;
0; Mismatches 2;
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                                                                                                              FastSEQ for Windows Version 3.0
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 211
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US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
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Patent No. 6297367
GENERAL INFORMATION:
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ilarity 98.9%;
Conservative
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Best Local Similarity
Matches 179; Conserv
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NUMBER OF SEQUENCES: 5

TITLE OF INVENTION:

Calzone, r.... Chang, Ming-Shi Chang, Ming-Shi OSTEOPROTEGERIN

Lacey, David L.

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RESULT 6
US-09-042-785A-12
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                                                                                                                                                                                                    Sequence 12, Application US/09042785A Patent No. 6194151 GENERAL INFORMATION:
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Best Local Similarity
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                 NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
NUMBERSE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               TITLE OF INVENTION: NOVEL MOLECULES OF THEREFOR AND USES THEREFOR
                                              ADD...
STREET: 2.
STREET: Massar
COMPUTER READABLE FORM:
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COUNTRY: UL.
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JENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
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Pred. No. 2.9e-31;
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Patent No. 6
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
                                                                                                                                                                                                                                                                  APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
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REFERENCE/DOCKET NUMBER: METELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: 1840 Dehavilland
CITY: Thousand Oaks
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                                                                                                                                                      COUNTRY:
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TOPOLOGY: linear
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77; Conserv
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(617)742-4214
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Pred. No. 2.9e-31;
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FILING DATE:
CLASSIFICATION:
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US-08-974-186-6
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                                                                                                                                                                                                                                                                                            74;
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Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74
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Patent No. 6284728
GENERAL INFORMATION
APPLICANT: Lacey, David L.
APPLICANT: Cacone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
RREPERENEY/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
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STREET: One Amgen Center Drive
CITY: Thousand Oaks
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET UNMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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US-08-795-447A-6
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                                                     Gaps
                                                                                                  5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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     Length 401;
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29.5%; Score 440.5; DB 4; Length 41.2%; Pred. No. 2.9e-31; ive 31; Mismatches 74; Indels
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ZIP: 9120-1789
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
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41.2%; Pred. No. 2.9e-31;
iive 31; Mismatches 74;
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTEGERIN
UMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
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amino acid
Query Match
Best Local Similarity 41.2%
Matches 77; Conservative
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Matches 77; Conservative
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MOLECULE TYPE: protein
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Best Local Similarity
"~* hes 77; Conserve
                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-795-446B-6
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 08/577,788
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                         VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145
                                                                                                                                                                        LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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EEAFFRF 209
                                  ERAVIDE 189
                                                                     PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC
                                                                                                      PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74; Indels 5
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; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-1
                                                                ; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1
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APPLICANT: Michael R.
APPLICANT: Peter R.)
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APPLICANT: McDonnell, Peter C.
                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 1
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Best Local Similarity
Matches 77; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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Patent No. 62970
Query Match
Best Local Similarity
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CURRENT FILING DATE: 1998-09-16
EARLIER APPLICATION NUMBER: 60/061,334
EARLIER FILING DATE: 1997-10-08
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS
FILE REFERENCE: GH-50030
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PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
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                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GH50031
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  29.5%;
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74
  Score 440.5; DB 4;
Pred. No. 2.9e-31;
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RELATED RECEPTORS TR1 AND TR2
                  Length 401;
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NUMBER OF SEQUENCES:
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STATE: Ca
COUNTRY:
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 5; Gaps
                                                                     26 РКУЛНУОВЕТЅНОЛІСОКСРРСТУТКОНСТАКМКТУСАРСРОНУУТОЅМНТЅОВСІЛССР 85
                                  PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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74; Indels
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74
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US-08-706-945D-128
Sequence 128, Application US/08706945D
Sequence 128, Application US/08706945D
Sequence 128, Application US/08706945D
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR APPLICATION DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.1
 31; Mismatches
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
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LENGTH: 401
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Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                                                                                                                            ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
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40 Dehavilland Drive
                       1: Amgen Inc.
1840 Dehavilland Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Winter, Robert B.
REFERENCE/STOCKER: JINFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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                                  STREET: 1840 CTTY: Thousand Oaks
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Matches 81; Conserv
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ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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STREET: 18
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-2
Search completed: January 6, 2003, 11:21:35 Job time: 22 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
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                                                                                                                      183
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THIS PACE BLAMF (USOPO)

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLDXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-MANL_TIMEOUT=30 -THREADS=1 -XGAPOPT_0 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Perfect score:
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Maximum DB
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3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
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ID AAZZ
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AAC AAZZ
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DT 17-C
DT 17-C
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Huma
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17-DEC-1999

(first

entry)

AAZ25377 standard;

CDNA;

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ALIGNMENTS

Human mFLINT #1 nucleotide sequence.

Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; Fash; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; growth, myelodysplastic syndrome; pancytopenic condition:

Homo sapiens.

myocardial ischaemia; ss

SUMMARIES

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Human, FAS Ligand Inhibitory Protein, FLINT; analogue; apoptosis; tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis; acute respiratory distress syndrome; ulcerative colitis; chronic obstructive pulmonary disease; crohn's disease; ss.
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AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTTGGAGCAC
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                                                    AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis
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Noblitt TW, Reidy
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Kharitonenkov A, Mizrahi J, Na S,
Wang J, Wu X, Zuckerman SH;
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                                                                                                                   98US-0079856.
98US-0086074.
98US-0112577.
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09-SEP-1998;
17-DEC-1998;
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22-DEC-1998;
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Newton CM,
Wroblewski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a mature human FAS Ligand Inhibitory Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature Protein protein is modified to produce analogues, which have greater potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
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                                                                                                    CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln
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Noblitt TW,
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26-JAN-2000;
The present sequence is that of cDNA coding for human FAS ligand inhibitory protein FLINT mature protein (see AAB19705). FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with FAS. This interaction is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis. The invention relates to novel FLINT
                                                                                                                       Novel protease resistant FAS ligand inhibitory protein resistant to in vivo or in vitro proteolysis at amino a of the mature protein, useful for treating autoimmune of
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analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence.

Mucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT cDNA is used as a template for introducing the required point mutations e.g. via PCR mutagenesis. The protease resistant FLINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, chronic obstructive pulmonary disease, pulmonary fibrosis, to inhibit T lymphocyte activation, and to facilitate organ preservation for transplantation (claimed).
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Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and prevents FasL-Fas mediated apoptotic and pro-inflammatory activity. WFLINT inhibits FasL-Fas mediated apoptotic and pro-inflammatory activity. WFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting ulcerative collist, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation. WFLINT abnormal (Mepatocyte) apoptosis, seppls, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, hyper indiabetes, cancer, damage to an innocent pystrander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
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GGGGGCTGCTGCTGGCGGCTGCTGCTGCAGGCGCTGCCCAGGATGCCCGGGCTGGAG
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Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
                                        Human mature fas ligand inhibitory protein (FLINT) cDNA.
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acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy; chronic obstructive pulmonary disease; COPD; acute lung injury; goitre; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diseates mellitus (IDDM); inflammatory bowel disease; Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; Down's syndrome; multiple sclerosis; cytostatic; nootropic; neuroprotective; vasotropic; ss.
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/product= "Human mature fas ligand inhibitory protein
(FLINT)"
/note= "CDS does not include start and stop codon"
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07-DEC-1999; 07-DEC-1999; 07-DEC-1999; 23-MAR-2000; New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked P-PSDB; AAE03567. Lu J, (ELIL) LILLY 2001-381684/40 Witcher DR; ; 99US-0169367. ; 99US-0169381. ; 99US-0169412. ; 2000US-0191430. S S ELI.

29-NOV-2000;

2000WO-US30166

Example 1; Page 53; 60pp; English

The present sequence is human mature fas ligand inhibitory protein (FINIT) cDNA, FLINT, a homologue of tumour necrosis factor receptor protein (TNPR), binds fas ligand (FasL) and thereby preventing the contraction of FasL with fas. FLINT comprising O-linked or N-linked colligosaccharides is useful for preventing or treating acute lung injury (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis, correctly pulmonary disease (COPD) and pulmonary fibrosis (PF), correctly contracted pulmonary disease (COPD) and pulmonary fibrosis (PF), correctly contracted pulmonary disease (COPD) and pulmonary fibrosis (PF), correctly contracted pulmonary fibrosis (PF), correctly contracted preservation for transplantation and to inhibit T (Inguise) as rheumatoid arthritis, fibroproliferative lung disease, correctly, inchaemia, brain trauma/injury, chronic renal failure, graft-vs-host disease, cutaneous inflammation, vascular leak syndrome, helicobacter pylori infection, goitre, atherosclerosis, insulin dependent C diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease such as C Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as C peoriasis, Down's syndrome, and multiple sclerosis.

Sequence 813 BP; 122 Þ 298 Ç; 267 ဂ္ 126 H 0 other;

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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
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multiple organ dysfunction; MODS; human; gene;

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                    ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys
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The invention relates to a new method of administering FLINT administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS). The method minimises the pain and discomfort of injection methods. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                               Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -
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30-MAR-1998;
20-MAY-1998;
09-SEP-1998;
17-DEC-1998;
18-DEC-1998;
18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                              Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; Fash apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; growth; myelodysplastic syndrome; pancytopenic condition; myocardial ischaemia; ss.
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The present invention describes therapeutic applications of mature FLINT (C (mFLINT)) for use in the treatment of acute liver failure. Mature FLINT (C (mFLINT)), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal special sequences, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage or damage to an consider tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that the constant bystander tissue that is induced by a chemotherapeutic agent or therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
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TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
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The present sequence is the coding sequence of the human Fas ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific approass, and can be used to treat inflammatory and autoimmune diseases cuch as rheumatoid arthritis, inflammatory bowel disease, disease, fifections diseases disease, diabetes, psoriasis and Graves' disease, confections diseases such as HIV-induced lymphopenia, fulnimant viral hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated ulceration, ischaemia and reperfusion conditions including acute and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung injury and acute respiratory distress syndrome, congestive heart failure and atherosclerosis, and Alzheimer's and Parkinson's diseases, brain injury and acute respiratory distress syndrome, Crohn's disease, brain anaemia, myelodysplasia, ulcerative collitis, Down's syndrome, and multiple sclerosis. In addition, the gene and protein can be used to prevent apoptosis following organ transplantation.
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         Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which binds Fast and LIGHT a prevents Fast-Fas interaction. Mature FLINT (mFLINT) inhibits Fast-Fas mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
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                                       CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCACGAC
                                                         ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
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                                                                                                                                                                                                                                                                                                           HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human; tumour necrosis factor receptor; muscle disorder; bone mass; screening; muscle metabolism; binding agent; cognate ligand; ss.
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Tumour necrosis factor receptor; TNFR-Galpha; TNFR-6beta; therapy; immune system-related disorder; inflammatory disease; immunosuppressive; bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; autlipe solerosis; Crohn's disease; autoimmune encephalitis; allergy; graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis; neuroprotective; antiarteriosclerotic; dermatological; asthmitis;
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                                                                                                              CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
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21-NOV-2000;
06-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human tumour necrosis factor receptor (TNFR)-falpha and 6beta protein and their corresponding nucleic acids. The invention provides screening methods for identifying agonists and antagonists of TNFR-falpha and 6beta activity. The invention also provides diagnostic and therapeutic methods for detecting and treating immune system-related disorders. The method is useful for treating or preventing an inflammatory disease or disorder selected from bowel disease, encephalitis, atherosclerosis and psoriasis, an autoimmune disease or disorder selected from systemic lupus crythematosus, arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, and autoimmune encephalitis, graft versus host disease (GVHD), and an allergy or asthma. The present sequence is Mammalian synthetic TNFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecules comprising a polynucleotide encoding huma tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides useful for treating disease e.g. inflammatory and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 903
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TGCCAGCCCTGTCCTCGGCACCTTCTCTGCATCTAGCTCCAGCTCTGAACAATGCCAA
                                                 GCTTCTTGTCCTCCTGGTGCTGGAGTGATCGCTCCTGGTACACCCTCTCAGAACACCCAA
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The present sequence encodes the tumour necrosis factor (TNF) receptor polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiency syndrome (AIDS) anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,
                                                                                                rejection
                                                                                                           New tumor necrosis factor receptor, NTR3, useful for treating cancers, stroke, anemia, obesity, rheumatoid arthritis and transplantation
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sick syndrome, hademorrhagic shock, hepatitis, insulin resistance, beloves, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia, obesity, rejection of transplanted organs, rheumatoid arthritis, septic shock syndrome, stroke, adult respiratory distress syndrome (ARDS), tuberculosis, and a number of viral diseases. The NYR3 polypeptide is beful for identifying or developing new (ant) agonists of NYR3. It may be used as an immunogen to which antibodies may be raised. NYR3 nucleic acid molecules may be useful as hybridisation probes in diagnostic assays to test, either qualitatively or quantitatively, for the presence of an NYR3 DNA or corresponding RNA in mammalian tissue or bodily fluid samples.
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The MGB protein is a member of a family of proteins which have roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. MGB lacks a transmembrane domain stimulation of cell differentiation. MGB lacks a transmembrane domain can is a secreted factor suggesting that it functions as a natural multitude of tissues suggests that MGB may play a role in cancer by inhibitor for its ligand. The altered expression pattern of MGB in a multitude of tissues suggests that MGB may play a role in cancer by such a ligand. This anti-apoptopic role of MGB suggests that modulators of MGB will be useful in treatment of apoptosis. The diseases such as various forms of cancer and various bone disorders. MGB nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying cancer and other diseases associated with abnormal levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteoporosis, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                         M68; tumour necrosis factor; TNF; programmed cell death, apoptosis, receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis; Crave's disease; idiopathic myxodema; multiple sclerosis; thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcerative colitis; glomerulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemia; myelodisplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
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GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu
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                                                                                                         The present sequence represents the human tumour necrosis factor creceptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides for the TNFR-6 beta cDNA (ANY9086). TNFR-6 alpha and TNFR-6 beta are members of the tumour necrosis factor receptor (TNFR) family. TNFRs care expressed in endochelial cells, keratinocytes, normal prostate and prostate tumour tissue. For a number of disorders of these cells, carticularly of the immune system, substantially altered (whether increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR-6 alpha and TNFR-6 beta genes can also be detected. The TNFR polypeptides are claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
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                                                                 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr
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ints sequence encouses the invention. The TNFR-falpha and TNFR-fabet DNA and protein sequences can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate TNFR expression. The nucleic acids, polypeptides, antibodies, agonists and antagonists against them may be used for the treatment of a range of conditions such as diseased with neovascularisation (sepecially coular neovascularisation) (sepecially coular concert, breast cancer and colon cancer), diabetic retinopathy conditions ascolated opthalmopathy tissue/cell damage, wounds, microbial and parasitic infections, bone disease (e.g. osteoporosis), atheroscierosis, pain, cardiovascular disease (e.g. osteoporosis), allorders (e.g. disorders (e.g. Albeimer's disease), immune disobetes, asthma, psoriasis, septic shock and ulcerative
                   bone disease; osteoporosis; atherosclerosis; cardiovascular disease; heurodegenerative disorder; Alzheimer's disease; immune disorder; graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma; psoriasis; septic shock; ulcerative colitis; therapy; ds.
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99US-0131279.
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30-APR-1999;
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260	241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu	
831	772 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCACGAC	
240	221 ArgalaalaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyalaGlnAsp	
771	712 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC	
220	201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly	
711	652 GAGTGTGAGCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG	
200	181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu	
651	592 GACACCCTGTGCACCAGCTGCACTGCCCCCTCAGCACCAGGGTACCAGGAGCTGAG	
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591	532 CCCCACGCAACTGCACGGCCCTGGGCCCTCAATGTGCCAGGCTCTTCCCAT	
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531	472 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGCTCCAG	
140	121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln	
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120	101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln	
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100	81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis	
351	292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGACGGGCTTGCCACGCCACCCAC	
80	61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis	
291	232 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC	
60	ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysAr	
231	172 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGAGACAGCCCCACGACG	
40	21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr	

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(c) 1993 - 2003 Compugen Ltd
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P25943 shope fibro
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P43489 homo sapien
P15725 rattus norv
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SEQUENCE FROM N.A. TISSUE=Lung; MEDLINE=20122600; PubMed= Bai C., Connolly B., Metz Soderman A., Galloway S.M "Overexpression of M68/Dc independent of gene ampli cluster."; Proc. Natl. Acad. Sci. U. [4] SEQUENCE FROM N.A. Matthews L.; Submitted (NOV-2000) to t [5] SEQUENCE FROM N.A. TISSUE=Lung; STABUSELUNG; SUBMITTION: Decoy recep and TMFSF6/FasL. Prot -i- TISSUE SPECIFICITY: D	SEQUENCE FROM N.A. TISSUB=Fetal lung; MEDLINE=99087326; PubM Pitti R.M., Marsters S Dowd P., Huang A., Don Godowski P.J., Wood W. Goddard A.D., Botsrein "Genomic amplification colon cancer."; Godowski P.J., Wood W. Goddard A.D., Botsrein "Genomic amplification colon cancer."; POSTUBLE SPOSTATE; SEQUENCE FROM N.A., AN TISSUB=Prostate; MEDLINE=99253915; PubM YU K.Y., Kwon B., Ni "A newly identified me superfamily (TR6) supp J. Biol. Chem. 274:137	HUMAN TR6B_HUMAN TR6B_HUMAN TR6B_HUMAN TR6B_HUMAN TR6B_HUMAN TS-JUN-2002 (Rel. 4 TS-JUN-2002 (Rel. 4 TS-JUN-2002 (Rel. 4 TS-JUN-2002 (Rel. 4 TNUOR DECROSIS FACT TREESFOB OR DCR3 OR HOMO Sapiens (Human Eukaryota, Metazoa, Mammalia; Eutheria; MCBI_TAXID=9806;	155.5 155.5 152.5 151.5 114.5 148.5 148.5 147.5 147.5 143.5 1142.5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon
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TURRE-CYS 1.
TURRE-CYS 2.
TURRE-CYS 4.
BY SIMILARITY.
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Prodom; PD00071; TNFR c6; 1.
SMART; SM0208; TNPR; 3.
PROSITE; PS0052; TNFR NGFR 1; 2.
PROSITE; PS0050; TNFR NGFR 2; 2.
Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
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Pred. No. 1.1e-110;
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AF217793; AAF33685.1;
AF217794; AAF33686.1;
AL121845; CAC03668.1;
BC017065; AAH17065.1;
W; HGNC:11921; TNFRSF6B.
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Best Local Similarity 100.
Matches 271; Conservative
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Shimamoto G.,
Sullivan J.,
Pattison W.,
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MEDLINE-98151033; PubMed=9492069;
MEDLINE-98151033; PubMed=9492069;
Vasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
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Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Kidney;

MEDLINE=9726201; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Lacey D.L., Dunstan C.R., Selley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
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Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density."
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                       T11B HUMAN STANDARD; PRT; 401 AA.
000300; 060236; Q9UHP4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98351569; PubMed=9688283; Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K "Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.";
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245:382-387 (1998)
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MEDLINE=98238645; PubMed=9571159;
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RESULT 2
T11B_HUMAN
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specifically inhibits osteoclastogenesis.";

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REPRESENTATION OF TRANSPORTED BY A CONTRACT O
                                                                                   InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                           EMBL; AB008822; BAA32076.1;
EMBL; AB008821; BAA332076.1;
EMBL; BC030155; AAH30155.1;
EMBL; AF134187; AAF20168.1;
HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverm Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James I.E., Rosenberg M., Lee J.C., Young P.R.; "Ostcoprotegerin is a receptor for the cytotoxic ligand TRAIL."; J., Biol. Chem. 273:14363-14367(1998).
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Morinaga T., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98148058; PubMed=9478964;
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                                                                                                                                                                                                                                                                      MIM; 602643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
   PROSITE; PS50017;
PROSITE; PS00652;
PROSITE; PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow. Detected at very low levels in brain, placenta and skeletal muscle. Highly expressed in fetal kidney, liver and lung. INDUCTION: Upregulated by increasing calcium-concentration in the medium and estrogens. Downregulated by glucocorticoids. PTM: N-glycosylated. Contains sialic acid residues. SIMILARITY: CONTAINS 4 TMFR-CYS REPEATS.
SIMILARITY: CONTAINS 2 DEATH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                 AB002146; BAA25910.1; -.
AB008822; BAA32076.1; -.
AB008821; BAA32076.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U94332; AAB53709.1; -.
                                                                                                                                                                                                                                                                                                  HGNC:11909; TNFRSF11B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                             AAF20168.1; -.
; DEATH_DOMAIN;
; TNFR_NGFR_1; 2
; TNFR_NGFR_2; 2
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                                                    FALSE_NEG.
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SIGNAL
                                                                                               T11B_RAT STANDARD; PRT; 401 AA. 008727; 008727; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
DOMAIN
TISSUE=Embryonic intestine;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.
Luethy R., Nguyen H.Q., Wooden S., E
                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                 (Osteoprotegerin)
TNFRSF11B OR OPG.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                              NCBI_TaxID=10116;
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                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C
                                                                                                                                                                                                                                                                                                   PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV
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                                                                                                                                                                                                                                                                                                                                                  263
401
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401 M
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46040 MW;
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LOUIS A. CYS 3.
TNER-CYS 4.
DEATH 1.
DEATH 1.
DEATH 7.
NOV
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DEATH 2.
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MISSING: ABOLISHES
D -> A (IN REF. 1)
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Pred. No. 8.
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                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
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C.R., Kelley M., Ch
Bennett L., Boone
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HES DIMERIZATION
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Chang
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(POTENTIAL).
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                                                                 Euteleostomi;
                                                          Murinae; Rattus.
                                                                                                 precursor
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 M.-S.,
Shimamoto
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION (BY SIMILARITY).
BY SIMILARITY.
                                                                                                its function. Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRALL and protect against apoptosis. TRALL binding blocks the inhibition of osteoclastogenesis (By similarity).
-: SUBCELMILAR LOCATION: Secreted (By similarity).
-: INDUCTION: Upregulated by osteopontin.
-: SIMILARITY: CONTAINS 2 DEATH DOMAINS.
     Sullivan J.,
Pattison W.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Suggs S., Boyle W.J., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J., "Osteoprotegerin: a novel secreted protein involved in the regulation of bone denaity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUPERFAMILY MEMBER 11B.
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SMART; SM00005; DEATH; 1.

SMART; SM00006; DEATH; 1.

SMART; SM00208; TNFR; 4.

SMOSITE; PS50017; DEATH DOMAIN; FALSE_NEG.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH 1.
                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 1.
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N-LINKED
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InterPro, IPR001368; TNFR_c6.
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DOMAIN
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REPEAT
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"Osteoprofegerin reverses osteoporosis by inhibiting endosteal osteoclasts and prevents vascular calcification by blocking a process resembling osteoclastogenesis.";
J. Exp. Med. 192:463-474(2000).
-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial adloification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUB=Kidney;
STRAIN=BALB/C; TISSUB=Kidney;
SIMONE W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy B., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                        PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoclastogenesis inhibitory factor (OCIF) in embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga
                                                                                                         146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J., Simonet W.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                          precursor
                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor superfamily member 11B pr
(Osteoprotegerin) (Osteoclastogenesis inhibitory factor)
INFRSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                Tilb_MOUSE STANDARD; PRT; 401 AA. 008712; 070202; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                             ERAVIDFVAFQDISIKRLQRLLQAL 207
                                                                                                                                                                                                   EEAFFRFAVPTKIIPNWLSVLVDSL 227
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gene and its expression
Gene 215:339-343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 89:309-319(1997).
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Indels

86; DB 1; .3e-26;

28.5%; Score 425.5; D 39.5%; Pred. No. 1.3e-live 33; Mismatches

Query Match
Best Local Similarity 39.55
Matches 81; Conservative

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Length 401;

PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64 26 PKYLHYDPETGROLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

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Interpo, IPRUVILLA, C6; J.

R Interpo; IPRUVILLA, C6; J.

R Promom; PD00020; TNFR_C6; 1.

DR Probom; PD000771; TNFR_C6; 1.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00005; DEATH DOMAIN; 1.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS50050; TNFR_NGFR_1; 2.

DR PROSITE; PS50050; TNFR_NGFR_2; 2.

Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

PROSITE; PS50050; TNFR_NGFR_1; 2.

Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

Receptor; Apoptosis; Glycoprotein; MEMBER 11B.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB013898; BAA28269.1; -...
EMBL; AB013903; BAA33388.1; -...
EMBL; AB013899; BAA33388.1; JOINED.
EMBL; AB013890; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
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CARBOHYD
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                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,25-dihdroxyvitamin D3 and parathyroid SIMILARITY: CONTAINS 4 THER-CYS REPEATS. SIMILARITY: CONTAINS 2 DEATH DOMAINS.
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INDUCTION: Upregulated by TGF-beta and estrogens.
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brachiocephalic
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On day 15 found in developi
cephalic artery and ductus
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28.5%;
39.0%;
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ound in developing bone primordia,
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                 L -> ...
SWISS).
W; CAA6102D3B312470 (
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BY SIMILARITY
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              Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91045991; PubMed=2172983; Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King Kohno T., Brewer M.T., Thompson R.C., Vannice J.L.; Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor gene product onaturally occurring tumor necrosis factor inhibitor."; proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor necrosis factor receptor superfamily member necrosis factor receptor 2) (p80) (TNF-R2) (p75) (Contains: Tumor necrosis factor binding protein 2 TNFRSF1B OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96299745; PubMed=866
Beltinger C.P., White P.S.,
Lepaslier D., Stallard B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90260639; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solam L., E
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines
                                                                  SEQUENCE OF 116-461 FROM N.A., ANI MEDLINE=90349572; PubMed=2166946; Heller R.A., Song K., Onasch M.A.
                                                                                                                                                                "Two human TNF receptors have similar intracellular, domain sequences."; Cytokine 2:231-237(1990).
                                                                                                                                                                                                                                       Brockhaus M.,
                                                                                                                                                                                                                                                                                                                                                      "Physical mapping and genomic Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                          Brodeur G
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Science 248:1019-1023(1990).
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                                         Ringold
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E=91370690; PubMed=1966549;
Z., Loetscher H., Gubler U
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hite P.S., Maris J.M.,
llard B.J., Goeddel D.
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                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
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Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
                                                                         Engelmann H., Novick D., Wallach D.; The tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i. FUNCTION: Receptor with high affinity for INFSF2/INF-alpha and approximately 5-fold lower affinity for homotrimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                        Loetscher H., Schlaeger B.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
Brockhaus M.;
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                                                                                                                                                                                                                                                                                "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
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; U52165; AACS0622.1; -.
; U52156; AACS0622.1; JOINED.
; U52157; AACS0622.1; JOINED.
; U52158; AACS0622.1; JOINED.
; U52159; AACS0622.1; JOINED.
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143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVA----IPGNASMDA 198
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TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
EXTRACELLULAR (POTENTIAL).
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TURR.-CYS 1.
TURR.-CYS 2.
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PROSITE; PSSOUG50; TNFR NGFR 2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
SIGNAL 1
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-> R (IN REF. 2 AND 5).
-> T (IN REF. 5).
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603D0AE1CD69ACBF CRC64;
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Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:11917; TNFRSF1B.
MIM; 191191; -.
S63368; AAB19824.2;
M35857; AAA63262.1;
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PIR, B35010, B35010.
PIR, A23666, A2366.
PDB; 1CA9; 12-APR-99.
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TRIB_MOUSE STANDARD; PRT; 474 AA.

P25119; P97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A., "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wong G.H. "Cloning
     DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha approximately 5-fold lower affinity for homotrimeric TNFSF1/Lymphotoxin-alpha (By $1milarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91187885; PubMed=1849278;
Lewis M., Tartaglia L.A., Lee A..
                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M60469; AAA39752.1; -.
EMBL; M59378; AAA40463.1; -.
EMBL; U39488; AAA85021.1; -.
EMBL; X87128; CAA60618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacob C.O., Liu J.;
Submitted (JAN-1996) to the
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Jacob C.O.,
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                        Receptor;
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                                                                                                                                                                                                                          SP; P19438; INCF.
D; MGI:1314883; Thfrefib.
cerPro; IPR001368; TNFR_C6.
m; PF00020; TNFR_C6; 4.
DDom; PD000771; TNFR_C6; 1.
RT; SM00208; TNFR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A.
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                                                                                                                                            PS00652; TNFR_NGFR_1; 2.
PS50050; TNFR_NGFR_2; 3.
Transmembrane; Glycoprotein; Repeat; Signal.
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TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 1B. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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01-UN-1994 (Rel. 29, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
17-Unor necrosis factor receptor superfamily member 3
(Lymphotoxin-beta receptor) (Tumor necrosis factor r
protein) (Tumor necrosis factor C receptor).
LTBR OR TNFRSF3 OR TNFCR.
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                                                       Strausberg
                                                                                                                                                                                                  Baens M.,
                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=93252381; PubMed=8486360;
                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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16:214-218(1993).
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                                      (APR-2002)
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
                                   EMBL/GenBank/DDBJ databases
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Pred. No. 3.4
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                            related
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RESULT 8
TR21_MOUSE
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                                                                                                                                                                           MEDLINE=99223511; PubMed=10207006; Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.; Wu M.-Y., Wang Powen of the lymphotoxin-beta receptor mediates cell death in Hela cells."; J. Biol. Chem. 274:11868-11873(1999).
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20261554; PubMed=10799510;
Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A., Whitbeck J.C., Cohen G.H., Eisenberg N.J., Ware C.F.; read of the lymphotoxin-bera receptor is necessary and sufficient for LIGHT-mediated apoptosis of tumor cells."; J. Biol. Chem. 275:14307-14315(2000).

-: FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TNPS14/LIGHT. Promotes apoptosis via TRAF3 and LTB, and LTB and LTB and LTB and LTB and LTB and LTB arole in the development of lymphoid organs.
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Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM02008; TNFR, TNFR NGFR_1; 2.
PROSITE; PS50056; TNFR_NGFR_2; 3.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
               Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor."; Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Self-associates.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
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     MEDLINE=94225209; PubMed=8171323;
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Genew, HGNC:6718; LTBR.
MIM; 600979; -
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     RARAR REPRESENTATION OF THE PROPERTY OF THE PR
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Score 299.5; DB 1; Length 435; Pred. No. 1.2e-16;

20.1%;

Best Local Similarity

Query Match

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MEDITION.

Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;

Timparied C-un aninot terminal kinase activity and T cell

Timparied C-un aninot receptor 6-deficient mice.";

J. Exp. Med. 194:1441-1448(2001).

J. Exp. Med. 194:141-1448(2001).

J. Exp. Med. 194:148(2001).

J. Exp. Med. 194:141-1448(2001).

J. Exp. Med. 194:148(2001).

J. Exp. Med. 194:141-1448(2001).

J. Exp. Med. 194:148(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-1448(2001).

J. Exp. Med. 194:141-148(2001).

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J. Exp. Med. 194:141-148(194).

J. Exp. Med. 194:141-148(194).

J. Exp. Med. 194:141-148(194).

J. Exp. Med. 194:141-1448(194).

J. Exp. Med. 194:141-1448(194).

J. Exp. Med. 194:141-1448(194).

J. Exp. Med. 194:141-1418(194).

J. Exp. Med. 194:14
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                                                                                                                     EPOHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109
                                                                                                                                                                                   EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
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15-UNN-2002 (Rel. 41, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6).
      Gaps
                                                          13 ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F., Minami M.;
   Indels
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Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
"Murine DR6: murine TNFR-related death receptor-6.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            183 ERAVIDFVAFQDIS------IKRLQRLLQALEAPEGWGPTPRAG
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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   Mismatches 101;
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      Conservative
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PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
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EMBL; AY043489; AAK74193.1; -.
EMBL; BC016420; AAH16420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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SMART; SM00208; TNFR; 4.
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                                           173
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                                                                                   126
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CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
                                                                                                                                                                                                                                                TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:2151075; Tnfref21.
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ERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTE 234
                                                                                PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPL---STRVPGAEEC
                                                                                                                          CPWPMIERLPCAALTDRECICPPGMYQSNGTCAPHTVCPVGWGVRKKGTENEDVRCKQCA
                                                                                                                                                               CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 125
                                                                                                                                                                                                           TYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTRHENGIERCHDCSQP 112
                                           RGTFSDVPSSVMKCKAHTDCLGQNLEVVKPGTKETDNVC----GMRLFFSSTNPPSSGTV
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                                                                                                                                                                                                                                                                                                                    Similarity
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29.7%;
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                                                                                                                                                                                                                                                                                          Score 288.5; 1
Pred. No. 1.4e
32; Mismatches
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TNFR-CYS 2.
TNFR-CYS 3.
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EXTRACELLULAR (POTENTIAL).
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RESULT
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MEDLINE=98378343; PubMed=9714541;
Pan G., Bauer J.H., Haridas V., Wang S.
Aggarwal B.B., Ni J., Dixit V.M.;
"Identification and functional characte
domain-containing TNP receptor.";
FEBS Lett. 431:351-356(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_C6; 4.

ProDom; PD000771; TNFR_C6; 1.

SMART; SM00005; DEATH; 1.

SMART; SM00008; TNFR; 4.

PROSITE; PS0017; DEATH HOMAIN; 1.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                 - FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
- SUBCILIVIAR LOCATION: Type I membrane protein (Probable).
- SUBCILIVIAR LOCATION: Type I membrane protein (Probable).
- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.
- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member related death receptor-6) (Death receptor 6).
TNFRSF21 OR DR6.
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O75509; Q96D86;
                                                                                                                                        InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                    EMBL; BC017730; AAH17730.1;
EMBL; BC010241; AAH10241.1;
                                                                                                                                                                                                                                                   EMBL; AF068868; AAC34583.1; EMBL; AL096801; CAB75692.1;
                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
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"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
11-0TM-2002 (Rel. 41, Last annotation update)
11-0TM - necrosis factor receptor superfamily member 3 precursor
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MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CVB; TISSUE=Lung;
MEDLINE=96072804; PubMed=7594541;
Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
             TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 21.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 655;
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                                                                            CYTOPLASMIC (POTENTIAL)
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34.3%; Pred. No. 1.8e-15;
iive 23; Mismatches 88;
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LTBR OR TNFRSF3 OR TNFCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 CSRCPPGEFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLG--FEEVAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 HATHNRACRCRTGFFAHAGFCL----EHASCPPGAGVIA-PGTPSQNT------QCQP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 CPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R EMBL; U29173; AAA68964.1; -.
R EMBL; U30798; AAB10346.1; -.
R EMBL; U30798; AAA81334.1; -.
HSSP; O14763; LDDr.
R HSSP; O14763; LDbr.
R DITELPRO; IPRO01368; TNFR_C6.
R PÉGM; PO000071; TNFR_C6; 3.
R PROSITE; PS00622; TNFR, 3.
R PROSITE; PS00622; TNFR_NGFR_1; 2.
R PROSITE; PS0062; TNFR_NGFR_2; 3.
R PROSITE; PS0062; TNFR_NGFR_2; 3.
R PROSITE; PS0062; TNFR_NGFR_2; 3.
R PROSITE; PS50050; TNFR_NGFR_2; 3.
R RECEPTOR; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
T SIGNAL
                                                             FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARAC 76
"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 CKPGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICK-----NPPEPGAMLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CUTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%; Score 265.5; DB 1; Length 415; 30.9%; Pred. No. 5.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Indels
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29B326A566AEF661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                             -!- SUBUNIT: Self-associates (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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AILLSLVLFLLFTTVLACAWMRHPSLCRKLGTLLK--RHPEGEESPPCPAPRA 275

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CRMB VARV STAN
P34015; Q89098; Q85
01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
15-JUN-2002 (Rel. 4
                          This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute the modification of TNF-mediated antiviral processes (By
                                                                                                                                                                                                                                                                                            STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20107289; PubMed=10639322;
Shchelkunov S.N., Totmenin A.V., Loparev V.N.,
Gutorov V.V., Chizhikov V.E., Knight J.C., Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Garcia-1966, and Somalia-1977;
Massung R.F., Loparev V.N., Knight J.C., Ortmenin A.V., Shchelkunov S.N., Esposito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R., Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V Kelivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
EMBL; .X69198; CAA49137.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Garcia-1966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smallpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective mechanisms."; FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=India-1967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=India-1967 / Isolate Ind3;
MEDLINE-93202281; PubMede8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to
protective mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Potential
                                                                                                                                                                                                                                                                                                                                                                                'Alastrim smallpox variola minor virus genome DNA sequences.";
                                                                                                                                                           similarity).
SUBCELLULAR LOCATION: Secreted (By similarity).
SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tial virulence determinants in terminal regions of variola ox virus genome."; 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G2R OR
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
receptor II precursor (cytokine response modifying protein
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Q85407; Q89118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
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                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chizhikov V.E.,
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                                                                                                             collaboration
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RESULT 12
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EMBL; L122579; AAA60933
EMBL; U18339; AAA69467
EMBL; U18341; AAA69467
EMBL; Y16780; CAB54798
EMBL; U881146; AAB94377
EMBL; U881148; AAB94377
EMBL; U881149; AAB94377
EMBL; U88152; AAB94377
EMBL; U88152; AAB94377
FIR; D36858; D36858
PIR; S35987; S35987.
PIR; S46888; S46888.
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PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Glycoprotein; Repeat; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProDom; PD0000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
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                                                     207
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                                                                       GAE
                                                                                          DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL
                                                                                                             NTOCOPOPPGTFSASSSSSSSCOOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP
                                                                                                                                 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG
                                                                                                                                                    VLCGEREEEARACHATHNRACRCRTGFF----AHAGFCLEHASCPPGAGVIAPGTPSQ
                                                                                                                                                                        PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN
                                                                                                                                                                                          PIYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN
                                                                                                                                                                                                                         Similarity
                                                                      180
                                                                                                                                                                                                                                                      349 AA;
                                                                                                                                                                                                                                                                                                       182
274
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                     165
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31
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86
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173
1189
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2189
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AAA69933.1;
AAA6947.1;
AAA69467.1;
CAB54798.1;
AAB94377.1;
AAB94377.1;
AAB94377.1;
AAB94377.1;
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335
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32.2%;
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N-LINKED (GLCNAC...
                                                                                                                                                                                                              Score 260; DB
Pred. No. 1.3e
26; Mismatches
                                                                                                                                                                                                                                                                                            GARCIA-1966).
E -> K (IN ST
A -> E (IN ST
N -> D (IN ST
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GARCIA-1966)
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                                                                                                                                                                                                                                                      D45D40B5C6E780EF
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(IN STRAINS BUTLER-1952, GARCIA-(IN STRAINS BUTLEP - 1966)
                                                                                                                                                                                                                                                                          (IN STRAINS
                                                                                                                                                                                                                                                                                            (IN STRAIN SOMALIA-1977)
(IN STRAIN SOMALIA-1977)
(IN STRAINS BUTLER-1952
                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                         BUTLER-1952
                                                                                                                                                                                                                                                                                                                                                                          .) (POTENTIAL).
.) (POTENTIAL).
BANGLADESH-1975
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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STANDARD;

PRT;

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ATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
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HSSP; 014763; 1D0G,
InterPro; 1PR0013168; TNFR_c6.
SMART; SM00209; TNFR_6; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00506; TNFR_NGFR_1; 2.
PROSITE; PS00506; TNFR_NGFR_2; 3.
PROSITE; PS00506; TNFR_NGFR_2; 3.
SIGNAL.
119 POTENTIAL.
                                                                                                                                                                                                                                        351
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                                                                                                                                                                                                                                                                                                                                                                             (CRMB1 OR D2L) AND (CRMB2 OR H4R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y11842; CAA72578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 243:432-460(1998).
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   (CPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Orthopoxvirus.
NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
32
44
70
70
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CRMB_COWPX
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              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
5-JUN-2002 (Rel. 41, Last amnotation space)
Soluble TNF receptor II precursor (cytokine response modifying protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contribute to
                                                                                                                                                                                                                                                                             STRAIN=CMS;
PubMed=11907336;
Gubser C., Smith G.L.;
Gubser C., Smith G.L.;
"The sequence of camelpox virus shows it is most closely related to variola virus, the cause of smallpox.";
J. Gen. Virol. B3:855-872 (2002).
                                                                                                                                    Camelpox virus (strain CMS), and Camelpox virus (strain M-96). Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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SOLUBLE TNF RECEPTOR II.
TURE-CYS 1.
TWEN-CYS 2.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                  (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
"The genome of camelpox virus.";
submitted (COT-2001) to the BMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for TNR-alpha and TNR-beta. May contrithe modification of TNR-mediated antiviral processes (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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EMBL; AY009089; AAG37718.1; --
EMBL; AF438165; AAL73920.1; --
INTERPO; IPR001368; TNFR_G6.
Pfam; PF00020; TNRR_G6, 2.
SMART; SM00208; TNFR_7; 3.
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NCBI_TaxID=203172, 203173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
55-JUN-2002 (Rel. 41, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein
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Hu F.Q., Smith C.A., Pickup D.J.;

Hu F.Q., Smith C.A., Pickup D.J.;

Secreted form of the type II TNF receptor.";

Virology 204:343-356(1994).

-! FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes.

-! SUBCELDUAR LOCATION: Secreted.
-! SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=GRI-90 / Grishak;
MEDLINE=98229462; PubMed=9568042;
MEDLINE=98229462; DubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.; and right species-specific
"The genomic sequence analysis of the left and right species-specific
terminal region of a cowpox virus strain reveals unique sequences and
a cluster of intact ORFs for immunomodulatory and host range
102 TTHNRICECSPGYYCILKGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Best Local S
Matches 59
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SEQUENCE FROM N.A.

MEDLINE=97306336; PubMed=9162061;

Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-

Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,

Porter T.G., Trunch A., Young P.R.;

Porter T.G., Trunch A., Young P.R.;

"A newly identified member of the tumor necrosis factor receptor

"A newly identified member of the tumor and involvement in
                                                                                                                                                       Zhang W.,
Submitted
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                                                                                                                                                                                                        superfamily with a wide tissue distribution lymphocyte activation.";
J. Biol. Chem. 272:14272-14276(1997).
                                                                                                                                                                                                                                                                                                                                       Montgomery R.I., Warner M.S., Lum B.J., & "Herpes simplex virus-1 entry into cells the TNF/NGF receptor family."; Cell 87:427-436(1996).
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 [Herpesvirus entry mediator A) (Tumor necrosis factor
            SEQUENCE FROM
TISSUE=Skin;
                                                                                                    Struyf F., Posavad
                                                                                                               SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND MEDLINE=21629477; PubMed=11756979;
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TISSUE=Cervical adenocarcinoma;
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Mammalia; Eutheria;
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                                               "Search for polymorphisms
Nectin-1, and Nectin-2 in
. Infect. Dis. 185:36-44
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EMBL; U81232; AAD00505.1; --
EMBL; AF153978; AAP75588.1; --
EMBL; AF373877; AAL47717.1; --
EMBL; AF373878; AAL47718.1; --
EMBL; AF073878; AAL47718.1; --
EMBL; AF073878; AAL47798.1; --
EMBL; AF073794; AAH02794.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the [6]
                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                       CHAIN
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een the Swiss Institute of Bioinformatics and the EMBL outs
European Bioinformatics Institute. There are no restrictions
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Similarity 37.3 56; Conservative
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/FTId=VAR_013007.
                                                                                                                                                                                                                     CYTOPLASMIC TNFR-CYS 1. TNFR-CYS 2. TNFR-CYS 3.
Score 244; DB 1;
Pred. No. 1.8e-12;
4; Mismatches 68
                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
                                            /FTId=VAR 013440.
46CE13C2C70242C1
                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                     (GLCNAC.
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                     Length 283;
                                              CRC64;
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 Indels
                                                                                                      (POTENTIAL)
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Search completed: January
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             familial expansile osteolysis.";
Nat. Genet. 24:45-48(2000).
-!- FUNCTION: Receptor for THSF11/RANKL/TRANCE/OPGL; essential for FANKL." mediated osteoclarustogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.
-!- SUBSCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: UBLOUITOUS EXPRESSION WITH HIGH LEYBLS IN SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: DEFECTS IN TWFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND LOSS OF DENTITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN THFRSF11A ARE A CAUSE OF FAMILIAL PAGET DISEASE OF BONE 1. ALSO KNOWN AS PAGET DISEASE OF BONE 2 (FDB2). IT IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILATIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
                                                         77 HATHNRACRCRIGFFA-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ϋ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
                                                                          CPKCSPGYRVKBACGELTGTVCEPCPPGTYIAHLNGLSKCLOCOMCDPAMGLR--ASRNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H., Yano
 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLER---CRYCNVLCGEREEARAC
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                              i6-OcT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NP-KB) (Osteoclast differentiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hughes A.B., Ralston S.H., Marken J., Bell C., MacPherson H., Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Dendritic cell;
MEDITNE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda Nakagawa N., Higashio K., Morinaga T., Higashio K., Morinaga T., the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis."; Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                                                                                                                                                                                       616 AA.
                                                                                                                   131 ASSSSSEQCQPHRNCTALGLALNVPGSSSH 160
                                                                                                                                             -PNGTLEECQHQTKCSWLVTKAGAGTSSSH 200
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                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                        INFRSF11A OR RANK.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       TR11 HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 CNKCEPGKYMSSKCTTTSDSVCLPCGPDEYLDSWNEEDKCLLHKVCDT--GKALVAVVAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 NSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TURE CLES 4.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         SHAGNITE; PS00652; TWFR NGFR 1; 1.
PROSITE; PS00509; TWFR_NGFR_2; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC
AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL. SIMILARITY: CONTAINS 4 THFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
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/FIId=VAR_011516.
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E3DE9A7A08196F81 CRC64;
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SUPERFAMILY MEMBER 11A.
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Pred. No. 1.9e-11;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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Pfam; PF00020; INFR_c6; 4.
Probom; PD000771; INFR_c6; 1.
SMART; SM00208; INFR; 4.
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Genew; HGNC:11908; TNFRSF11A.
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Result
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-DB=_Issued_Patents_NA_-QFMT=fastap_-SUPFTX=ppn.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0-UNITS=Db1ts -STRAT=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODB=_LOCAL -OUTFMT=pto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09936024_@CGN_1_1_25_@runat_06012003_111607_12151 -NCPU=6 -ICPU=3
-NO XLDXY -NO MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Perfect score:
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US-08-795-4468-5
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Sequence 18, Appl
Sequence 19, Appli
Sequence 7, Appli
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quenc	equence 11, App	equence 5, Appl	equence 3, Appl	equence 5, App	equence 3, Appl	5, Appl	equence 3, App	equence 7, Appl	equence 1, App	equence 7, Appl	equence 1, Appl	equence 7, Appl	equence 1, Appl	equence 3, Appl	equence 3, Appl	equence 1, Appl	equence 2, App	tent No. 539576	equence 1, Appl	equence 1, Appl	equence 3, App	equence 125, Ap	e 3, App	equence 3, Appl	e 3, Appl	quence 3, Appl	equence 3, Appl	equence 123, Ap	equence 1, App	equence 1, Appl	equence 1, Appl	equence 1, Appl

ALIGNMENTS

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Sequence 1, Applic Patent No. 5885800
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ZEP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: DISK
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PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
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APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 04-FE
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Mismatches:
Indels:
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                                                                                                                                           Length:
Matches:
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                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                           1.25e-109
1491.00
100.00%
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TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                          Sequence 18, Application US/09286529;
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley;
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAM;
FILE REFERENCE: 1408 003/200130 439C1
CURRENT APPLICATION NUMBER: US/09/286,529;
CURRENT FILING DATE: 1999-04-05;
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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TYPE: DNA
ORGANISM: Homo sapien
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Query Match:
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                                                   RESULT 2
US-09-286-529-18
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Sequence 19, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND TN
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION UMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
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TYPE: DNA
ORGANISM: Homo sapien
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ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
                         TGCCAGCCGTGCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
                                                                           AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
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                                                                                                                                                                                                                                                 Sequence 7, Application US/09286529; Sequence 7, Application US/09286529; Patent No. 6297367; GENERAL INFORMATION:
APPLICANT: Catherine Tribouley; TITLE OF INVENTION: NEW MEMBERS OF TWF AND TWF; FILE REFERENCE: 1408.003/200130.439C1; CURRENT APPLICATION NUMBER: US/09/286,529; CURRENT FILING DATE: 1999-04-05; NUMBER OF SEQ ID NOS: 25; SOFTMARE: FastSEQ for Windows Version 3.0; SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-936-024-1 (1-271) x US-09-286-529-7 (1-459)
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Patent No. 6015938
GENERAL INFORMATION: APPLICANT: Boyle, Willaim J. APPLICANT: Lacey, David L.
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Best Local Similarity:
Query Match:
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ORGANISM: human
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US-08-974-022-5
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105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-936-024-1 (1-271) x US-08-974-022-5 (1-1355)
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                          E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Winter, Robert B.
REPRERICE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1355 base pairs
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440.50
57.75%
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CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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STRANDEDNESS: single
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
LOCATION:
US-08-974-022-5
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                                                          US-09-936-024-1 (1-271) x US-08-795-445A-5 (1-1355)
                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                     Alignment Scores:
                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                    JS-08-795-445A-5
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                                                                                                                                                                                                                                                                                                                                                           NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B
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                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT
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                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro
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Lacey, David L.
Calzone, Frank J.
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Chang, Ming-Shi
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94..1296
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41.18%
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Matches:
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Indels:
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US-08-795-447A-5
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                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: 1)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteop
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STREET: One Amgen Center Drive
CITY: Thousand Oaks
          LENGTH: 1355 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                 FILING DATE:
                                                                                                                                                                               APPLICATION NUMBER:
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Calzone, Frank J.
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                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                        Length:
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Patent No. 6284740
GENERAL INFORMATION
APPLICANT: Lacey, David L.
APPLICANT: Lacey, David L.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STREET: California
COUNTRY: USA
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57.75%
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29.54%
                              CDS
94..1296
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Best Local Similarity:
Query Match:
DB:
MOLECULE TYPE:
              FEATURE:

NAME/KEY:

LOCATION:

US-08-795-447A-5
                                                                                          Alignment Scores:
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165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
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Mismatches:
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Matches:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
RREFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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29.54%
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STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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US-08-795-446B-5
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APPLICANT: Boyle,
APPLICANT: Lacey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCY > > - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
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STRANDEDNESS: single
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STATE: California
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                                   CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC 34
                                                                                                                                  ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
                                                                    ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
                                                                                                        CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC 288
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APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Fran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: 0=+----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                                     ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro
ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
                                       CCTGGTACCTAACAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC
                                                                        ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
                                                                                                               CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT
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                                                                                                                                                                                                                            125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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                                                                                                                                                                                                                                                                                     CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
                                                                                                                                                                                                                                                                                                                                                165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
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TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
FILE REFERENCE: A-496
CURRENT APPLICATION UNBER: US/08/997,918
CURRENT FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 47
LENGTH: 525
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Mismatches:
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Patent No. 6077689
GENERAL INFORMATION:
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42.86%
29.04%
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Query Match:
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US-08-997-918-47
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rgAla - -	ercy 	InPro	SArg	CAC	rrret				
ISDA:	lase	'ysg] : GCA	roHi	AAC.	SPTP				
Hist 	Hisz 	GlnC	GlnE	CGT	H187				2432 81
aThr racc	uGlu :::	in Thr 	nCys	GTG	rSer			о _е .	(ν ω
fisa]	7,48L6	lnas GTAP	11uG	CTCC	erSe			т# ц	
ACYSI ATGC	Phe(SerC GAAC	erSerGluGlnCysGlnProHisArgAsn	PAAAC	G178			Version	Length: Matches:
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LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 	ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro	ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 	erAlaSerSerSerS	ccisarcistrutricticaargaaacricsassaagercestisceraasacacaas	CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys			Application US/08974022 (6015938 FFORMATION: TT: Lacey, David L. TT: Lacey, David L. TT: Lacey, David L. TT: Calzone, Frank J. TT: Calzone, Ming-Shi TT: Calzone, Ming-Shi TT: Lacey David Library Thousand Oaks Thousand T	
uGlu. CGTT	eAla : :	aPro GGCT	aSer	CGAA	aleu GTTA			12 74-022-1 76-022-1 76-022-1 The of Japplication US/08974022 t No. 6015938 FLICANT: BOYle, Willaim J. PLICANT: Lacey, Willaim J. PLICANT: Calzone, Frank J. SEREPONDENCE ADDRESS: ADDRESSS: ADDRESSSS: ADDRESSS: ADDRESSS: ADDRESSSS: ADDRESSSS: ADDRESSSS: ADDRESSSSS	24
i i AGTA	hePh ::	leal :: Taca	erAl	CCAA	euAl - -			willaim willaim bavid L. Frank Ming-Sh. 63TEOJS: 53 EBSS: Compat. Prompty disj. ppy di	06e- 5.50
Argo	GIYE	Vall	ProProGlyThrPheS	TTCI				12 74-022-1 74-022-1 74-022-1 The of	1.
lyglu \GGAC	rgTh1	[ag] [] [CGG]	lyThi	TTT	laLeu			12 74-022-1 74-022-1 74-022-1 TO 6015938 RAL INFORMATION: No. 6015938 PLICANT: BOYLE, W: PLICANT: BOYLE, W: PLICANT: Calzone, Calyone, Cal	
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                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08795445A Patent No. 6284485
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                             APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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TYPE: nucleic acid
STRANDEDNESS: single
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GAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGGCTGAGTGTT
                            GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg
                                                                                          ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys
                                                                                                                                                         CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys
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                                                               TGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTCACCCTGTGC
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Matches:
Conservative:
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTEGERIN
WIMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN Inc.
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SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
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CLASSIFICATION
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
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ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE: CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE (TARRACTERISTICS:
LENGTH: 2432 base pairs
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Mismatches:
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APPLICANT: Lacey, David L.
APPLICANT: Lacey, David L.
APPLICANT: Clang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
                                                                                                                        Sequence 1, Application US/08795447A Patent No. 6284728 GENERAL INFORMATION:
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STRANDEDNESS: single
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Best Local Similarity:
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LOCATION:
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US-08-795-447A-1
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Search completed: January
Job time : 55 secs
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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US-09-935-727-1
US-09-896-096A-2
US-09-894-924-2
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rddu ' c compa	emience 9 April	equence 9, Appl	equence 17, App	equence 6, Appl	equence 6, Appl	equence 10, App	equence 10, App	equence 5, Appl	equence 5, Appl	equence 8, Appl	equence 97, App	equence 102, Ap	equence 84, App	equence 4, Appl	equence 1, Appl	equence 14, App	equence 1, Appl	equence 1164, A	equence 87, App	equence 86, App	equence 85, App	equence 6, Appl	equence 3, Appl	equence 94, App	enc	equence 10, App	equence 95, App	equence 93, App	equence 101, Ap	equence 96, App	equence 83, App	equence 92, App	equence 7, Appl	equence 3, Appl	equence 3, Appl	equence 3, Appl	ence 28, App	equence 19, App	equence 1, Appl	ence 33,	equence 18, App

ALIGNMENTS

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US-09-935-727-32

US-09-935-727-32

US-09-935-727-32

Sequence 32, Application US/09935727

Patent No. US20020150583A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REFERENCE: PP454P2

CURRENT APPLICATION NUMBER: US/09/935,727

CURRENT APPLICATION NUMBER: 00/303,224

PRIOR APPLICATION NUMBER: 60/303,224

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2000-11-21

PRIOR APPLICATION NUMBER: 60/252,131

PRIOR APPLICATION NUMBER: 60/257,598

PRIOR APPLICATION NUMBER: 60/257,598

PRIOR APPLICATION NUMBER: 00/257,598

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: 00/168,235

PRIOR FILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR FILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR FILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR FILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: 60/168,235

PRIOR FILING DATE: 1999-03-12-01
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41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
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US-09-935-727-1
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Matches:
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PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-14
PRIOR PILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 32
LENGTH: 903
TYPE: DNA
CREATER DNA
CREATER
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Sequence 1, Application US/09935727

Patent No. US20020150583A1

GENERAL INFORMATION:

TUTLE OF INVENDATION:

PRIOR APPLICATION NUMBER: 06/33,224

PRIOR FILING DATE: 2000-10-21

PRIOR PELICATION NUMBER: 06/227,588

PRIOR APPLICATION NUMBER: 06/18,331

PRIOR PELICATION NUMBER: 06/18,331

PRIOR PELICATION NUMBER: 06/146,371

PRIOR PELICATION NUMBER: 06/121,774

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APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAMRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIDE, CORTER TOWNS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIDE, CORTER TOWNSER: US/09/896,096A
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
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                                                                                                                                                                                                                                       AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
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                       GGGGCGCTGCTGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG
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     CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
                       TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGAGCAGCAGCAG
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Sequence 18, Application US/09877156
Sequence 18, Application US/09877156
Sequence 18, Application US/09877156
Settler No. US2002005625A1
Settler No. US2002005625A1
SPECTRAL INFORMATION:
TITLE OF INVENTION: NEW MEMBERS OF THY AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT PEPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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Best Local Similarity:
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BOTSTEIN, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: WERE MEDICANT: WIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENE, DAVID A.
APPLICANT: TURAS, DANIEL B
APPLICANT: TURAS, DANIEL B
APPLICANT: TURAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIOE
FILE REFERENCE: P1134R2 REVISED
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER: OF SEQ ID NOS: 18
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968 CGGAGCGTCCGTGAGCGCTTCCTCCTCTGCAC 1000
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                                                                                        Sequence 2, Application US/09894924
Patent No. US20020065210A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Unsure
COCATION: 1090
US-09-894-924-2
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Best Local Similarity:
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LENGTH: 1114
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FILE REFERENCE: PF454P2

CURRENT APPLICATION NUMBER: US/09/935,727

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/303,224

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2001-07-06

PRIOR PHILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: 60/252,131

PRIOR PHILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: 60/227,598

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-03

PRIOR PHILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: 60/146,371

PRIOR APPLICATION NUMBER: 60/146,371

PRIOR PHILING DATE: 1999-08-02

PRIOR PHILING DATE: 1999-08-02

PRIOR PHILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 60/131,270

PRIOR APPLICATION NUMBER: 60/131,270

PRIOR APPLICATION NUMBER: 60/131,270

PRIOR APPLICATION NUMBER: 60/124,092

PRIOR APPLICATION NUMBER: 60/124,092
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US-09-935-727-33
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PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR EILING DATE: 1998-01-13
PRIOR PILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: DATE: 1950
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Codon optimized TNF
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                                    AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr
ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
                                                                                              GAATGTGAAAGAGCTGTTATTGATTTGTTGCTTTTCAAGATATTTCTATTAAGAGACTG
                                                                                                              GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu
                                                                                                                                                      GATACTTTGTGTACTTGTACTGGTTTTCCTTTGTCTACTAGAGTTCCAGGTGCTGAA
                                                                                                                                                                     AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
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AGAGCTGCTTTGCAATTGAAGTTGAGAAGAAGATTGACAGAATTGTTGGGTGCTCAAGAT

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486 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCAGACACACGCAG
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CORGANISM: Homo sapien
US-09-877-156-19
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                                                                                                                               Sequence 1, Application US/09840795;
Patent No. US20020143147A1
GENERAL INFORMATION:
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Blizabeth Esther Mary
APPLICANT: Bates, Blizabeth Esther Mary
APPLICANT: Bates, Blizabeth Sther Mary
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related Reagents
FILE REFERENCE: SF0818K
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
SEQ ID NO 1
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FEATURE:
NAME/KEY: CDS
LOCATION: (99)..(998)
NAME/KEY: misc feature
LOCATION: (367)
OTHER INFORMATION: W; may be A or T
NAME/KEY: mat peptide
LOCATION: (132)..(998)
US-09-840-795-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
TATLE OF INVENTION: NEW MEMBERS OF TNF AND TNF
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT PILING DATE: 2001.06-08
PRIOR FILING DATE: 1998.04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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GCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTC	1305
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TCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTG 1004	945
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177	177
AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPro 177	645
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ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 16	141
TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCTCCAGGCTCCAGAGCAGTGCCAG	525
CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCys	121
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAG	465
AlaSarCvsProDroGlvAlaGlvValIleAlaDroGlvThrDroSerGlnBenThrGln 12	101
AsnArgAlaCyaArgCysArgThrGlyPhePheAllaHisAlaGyPheCysLeuGluHis 100 	405
TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCAC	345
TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 8	61
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PRIOR APPLICATION.

PRIOR PILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-04

PRIOR FILING DATE: 1999-03-04

PRIOR FILING DATE: 1998-03-04

PRIOR FILING DATE: 1998-01-13

PRIOR APPLICATION NUMBER: 60/035,496

PRIOR FILING DATE: 1997-01-14

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 28

LENGTH: 1796
; FEATURE:
; NAME/KEY: intron
; LOCATION: 425-560
; NAME/KEY: intron
; LOCATION: 756-1512
US-09-935-727-28
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR PELING DATE: 2000-07-06
PRIOR PPLICATION NUMBER: 60/252,131
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR APPLICATION NUMBER: 60/27,598
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILLING DATE: 2000-03-03
PRIOR PILLING DATE: 2000-03-03
PRIOR PILLING DATE: 1999-12-01
PRIOR PILLING DATE: 1999-12-01
PRIOR PILLING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR PILLING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR PILLING DATE: 1999-03-12
PRIOR PILLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR PILLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR PILLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/131,270
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US-09-935-727-28
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Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor
FILE REFERENCE: PF454P2
                                                                                                                                  LENGTH: 1796
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1725
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õ		177	177
qq	10	048	GGGAAACCGAGGCCTGATGGTAACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCT 1107
ò		177	177
qq	11	108	CTGACATGGGGAAACCGAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTG 1167
õ		177	177
q	11	168	ACCCCCTTAACATCAAGTCAGGTCCGGTCCCATCTGCAGGTCCCAACTCGCCCCTTCCGAT 1227
ò		177	177
qq	12	228	GGCCCAGGAGCCCCAAGCCCTTGCCTGGGCCCCCTTGCCTCTTGCAGGCCAAGGTCCGAGT 1287
ò		177	177
q	12	1288 GGCCGCTCCTGCCCCTAGGCCTTTGCTCCAGCTCTGAC	AGCTCTCTGACCGAAGGCTCCTGCCCCTTC 1347
ò		177	177
qq	Н	348 TCCAGTCCCCATCGTTGCACTGCCCT	CTCCAGCACGGCTCACTGCACAGGGATTTCTCTC 1407
õ		177	177
q	14	408	TCCTGCAAACCCCCCGAGTGGGGCCCCAGAAAGCAGGGTACCTGGCAGCCCCCCCC
ô		178	GlyAlaGluGluCysG 183
q	14	468	GTGTGGGTGAAATGATCGGACCGCTGCCTCCCCACCCCA
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රු පි	-	223 laLeuGlnLeuLysLeuArgArgL 	euThrGluLeuLeuGlyAlaGlnAspGlyAlaL 243
8 8	•	243 6	ArdSerV 26
3 음	1	1708 TGCTGGTGCGGCTGCTGCAGGCGCTGCGC	CCGGGCTGGAGCGGAGCG 17
ò		263 alArgGluArgPheLeuProValHis 271	
g	-	1768 TCCGTGAGCGCTTCCTCCTGTGCAC 17	93
N O O O O O O O O O O O O O O O O O O O	S-09-9 Seque Seque GENER APPL TILLE FILE CURR CURR CURR PRIO PRIO PRIO PRIO PRIO PRIO PRIO PR	SGUTT 10 -09-935-727-3 Sequence 3, Application US/09935727 SETEMBER 1 UNFORMATION: APPLICANT: Human Genome Sciences, In TITLE OF INVENTION: TUMOR NECROSIS F FILE REFERENCE: PF4542 CURRENT APPLICATION NUMBER: US/09/93 CURRENT FILING DATE: 2001-08-24 PRIOR PLING DATE: 2001-08-24 PRIOR PLING DATE: 2001-07-06 PRIOR PLING DATE: 2001-07-06 PRIOR APPLICATION NUMBER: 60/303,224 PRIOR PLING DATE: 2000-11-21 PRIOR APPLICATION NUMBER: 60/227,598 PRIOR PLING DATE: 2000-08-25 PRIOR FLING DATE: 1999-12-01	c. S.727

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PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/121,270
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1997-01-14
NUMBER: 09/580/015,496
PRIOR FILING DATE: 1997-01-14
NUMBER: 09/580/1D NOS: 42
SOPTWARE: PALENTIN VET. 2.1
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DB:
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                   135
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                                                                                                                                                                                                                                                                AlaSerCysProProGlyAlaGlyVallleAlaPro------
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rSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr
                                                                 oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSe
                                                                                                                                                                         GCCCCAGGAGTGGTCGGAGGTGTGGCAGGGTTCAGGTTGCTGGTCCCAGCCTTGCA
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                                                 CCCTGAGCTAGGACACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCC
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78.85%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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179
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APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUNAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIDE, A TNFR HOMOLOG
FILE REFERENCE: P112472 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US/09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/09896096A
Patent No. US20020661559A1
; GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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LENGTH: 491
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LOCATION: 62, 73, 8
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
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                    GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyVallleAlaProGlyThr 114
                                                                                          AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla
                                                                                                                                           TAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCGTGAGGAGGAGGCACGG
                                                                                                                                                                   TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArg
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 GGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACC
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Matches:
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Indels:
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Query Match:
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US-09-877-156-7
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ProSerGlnAsnThrGlnCysGln-ProCysProProGlyThrPheSerAlaSerSerSe
                   CAGCTCAGAGCAGTGCCAGCCCCAACTGCACGGCCCTGGGCCTGGCCCTCAATGT
                                                                                                           154 lProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerTh
                                                                                                                                      GCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC
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                                                       134 rSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVa
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GENERAL INFORMATION:

APPLICANT: BOTSTEIN, DAVID

APPLICANT: DOOGE, KELLY H.

APPLICANT: DOOGE, KELLY H.

APPLICANT: GENERAL ANSTIN L.

APPLICANT: GENERAL BAVID A.

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: PINAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: WOOD, WILLIAM I.

TITLE REFERENCE: P1134R2 REVISED;

CURRENT APPLICATION NUMBER: US/09/894,924

CURRENT FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: US 60/059,288

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 18

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Matches:
Conservative:
Mismatches:
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LOCATION: 62, 73, 86, 98
OTHER INFORMATION: unknown base
                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09894924
Patent No. US20020065210A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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ORGANISM: Unknown
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Pred. No.:
                                                                                                                                                                                                                                                                             RESULT 12
US-09-894-924-3
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                          GCTTGCCACGCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCT
                                                                                   GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr
                                                                                                            GGTTTCTGCTTGGAGCACGCATCGTGTCCTACCTGGTGCCCGGCGTGATTGCCCCGGGCACC
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75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla
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APPLICANT: Catherine Tribouley
TITLE OF INVENTOR: NEW MEMBERS OF TNF AND TNFR FAMILIES; FILE REFERENCE: 1408.003/200130.439C1
CURRENT PFLICATION NUMBER: US/09/877,156; CURRENT FILING DATE: 2001-06-08; PRIOR APPLICATION NUMBER: US 09/286,529; PRIOR FILING DATE: 1998-04-05; NUMBER OF SEQ ID NOS: 25; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 7;
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Mismatches:
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US-09-062-113-92
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FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REGERENCE/DOCKET NUMBER: FJN-060DV
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FBE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. US20020051969Alel Proteins and Methods for Producing TITLE OF INVENTION: the Proteins
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CITY: E
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ZIP: 02110
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125 High St.
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HIGASHIO, Kanji
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MORINAGA, Tomonori
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SHIMA, No. US20020051969Aluyuki
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MOCHIZUKI, Shin'ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOTO, Masaaki
TSUDA, Eisuke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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LOCATION: 1..981
COTHER INFORMATION:
US-09-062-113-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                        GACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCTCAGT
                                                                                      AlaLeuGlnLeuLysLeuArgArg---
                                                                                                                                                           LeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAla
                                                                                                                                                                                             GAAAACAGCGTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGC
                                                                                                                                                                                                                              GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg
                                                                                                                                                                                                                                                                  -----TGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATATTGACCTCTGT
                                                                                                                                                                                                                                                                                                   ThrSerCysThrGlyPheProLeuSerThrArgValProGly-----AlaGluGluCys
                                                                                                                                                                                                                                                                                                                                       TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATA---
                                                                                                                                                                                                                                                                                                                                                                      CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys
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   -GlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAla
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Matches:
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                                                                                                                          -CCGGGAAAGAAAGTGGGAGCAGAA
                                                                                      ArgLeuThrGluLeuLeu---
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124 435 144 315 104

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LOCATION: 1..1206
OTHER INFORMATION: /note= "(OCIF-C19S)"
US-09-062-113-83
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Job time : 136 secs
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Best Local Similarity:
                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                    Pred. No.:
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APPLICANT: TSUDA, EISUKE
APPLICANT: YANO, KAZUKI, Shin'ichi
APPLICANT: YANO, KAZUKI
APPLICANT: YANO, KAZUKI
APPLICANT: KOBAYASHI, Fumia
APPLICANT: SHIMA, No. US20020051969Aluyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: MAKGAMA, No. US20020051969Aluaki
APPLICANT: MORINAGA, Tomonori
APPLICANT: MORINAGA, Tomonori
APPLICANT: UEDA, Masatsugu
APPLICANT: UEDA, No. US20020051969Alel Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
---ACCTTGAAGGGCCTAATGCACGCA 819
                                                                                                                        820 chaaagcactcaaagacgtaccactttcccaaaactchcactcagagtctaaagaagacc 879
                                                            LeuArgValAlaArgMetProGlyLeuGluArgSerValArgGlu--
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FBB-1995
FILING DATE: 20-FBB-1995
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
FILING DATE: 20-FBB-1996
FILING DATE: 20-FBB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/JP96/00374
FILING DATE: 20-FBB-1996
APPLICATION NUMBER: JP 1996
ATTORNEY/AGENT INPORMATION:
NUMBER: APPLICATION DATA:
APPLICATION NUMBER: DCT/JP96/00374
FILING DATE: 20-FBB-1996
ATTORNEY/AGENT INPORMATION:
NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: DCT/JP96/00374
FILING DATE: APPLICATION DATE: DCT/JP96/00374
FILING DATE: APPLICATION NUMBER: DCT/JP96/00374
FILING DATE: APPLICATION DATE: DCT/
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve.
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
766 TTGTGGCGAATAAAAATGGCGACCAAGAC--
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REFERENCE/DOCKET NUMBER: F/N-060DV
TELECOMMUNICATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 83, Application US/09062113
Patent No. US20020051969A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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US-09-062-113-83
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                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, B. Mammalia, Butheria, Primates, Catarrhini, Hominidae, J. (basalia, to 813).

Lu, J. and Witcher, D.R.
Improving stability of flint through o-linked glycosy Patent: WO 1044643-A 2 14-JUN-2001,

ELI LILL AND COMPANY (US).

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 903)
Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Ebner,R. and Kwon,B.S.
A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis
J. Biol. Chem. 274 (20), 13733-13736 (1999)
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Direct Submission
Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635
Barnhill Drive, Indianapolis, IN 46202, USA
Location/Qualifiers
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Kwon, B.S. and Yu, K.Y.
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                                                                                                                                                                                                                         /note="similar to DCR3"
/codon_start=1
/product="tumor necrosis factor receptor homolog"
/protein_id="AAD29688.1"
/db_xref="GI:4768939"
/translation="WRALEGEGLSLICIVLALPALLEVPAVRGVAETPTYPWRDAETG
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T_lymphocyte"
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ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
SSSSBEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
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/tissue_type="pancreas"
53. 955
/note="TNFR; decoy receptor; DCR3; alternatively spliced"
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100.0%; Score 813; DB 9; Length 1
Best Local Similarity 100.0%; Pred. No. 6.6e-125;
Matches 813; Conservative 0; Mismatches 0; Indels
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Homo sapiens M68E mRNA, alternatively spliced, complete cds.
AP217794
AF217794.1 GI:6969262
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1048)

Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,

Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
Caskey,C.T.

Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
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Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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                      TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
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Sequence 1 from
AX082868
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1055)
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llarity 100.0%; Pred. No. 6.
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                        GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGTGC 60
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Sequence
AX055373
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Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J., Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L., Tumas,D., Watanabe,C.K. and Wood,W.I.
                                                                                                                                                                                       Patent: WO 0073452-A 3 07-DEC-2000; Genentech, Inc. (US)
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                                                               Similarity
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                                                   100.0%; llarity 100.0%; Conservative 0
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                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                        Location/Qualifiers
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WO0073452.
                                                   Score 813; DB 6;
Pred. No. 6.6e-125;
Mismatches 0;
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                                                                                  Score 813; DB 6; I
Pred. No. 6.6e-125;
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                                                                                 Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.6
Matches 813; Conservative 0; Mismatches
                                   191
/organism="Homo sapiens"
/db_xref="taxon:9606"
_379 c 356 g 191
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood,W.I.
Methods and compositions for inhibiting neoplastic cell growth
Patent: WO 0075316-A 1 14-DEC-2000;
Genentech, Inc. (US)
Location/Qualifiers
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Sequence 1 from Patent W00075316.
AX056645 GI:12309639
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

FEATURES

REFERENCE AUTHORS

DEFINITION ACCESSION

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RESULT 8 AX056645

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                                                                TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
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                                      TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
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1 (bases 1 to 1114)

Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C., Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T., Goddwski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L., Goddwski,P.J., Botstein,D. and Ashkenazi,A.

Genomic amplification of a decoy receptor for Fas ligand in lung
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Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
San Francisco, CA 94080, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DcR3"
/function="binds to Fas/Apo1/CD95 ligand and blocks its
activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="decoy receptor 3"
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101. .1003
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/db_xref="taxon:9606"
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REMAR COMMENT	OR OR REFE AU TI	RESULT 10 BC017065 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	g V2	g 8	B 8	8 8	g 8	g Q	용 성	상	상	В
REMARK	ORGANISM ORGANISM EFERENCE AUTHORS TITLE JOURNAL	SULT 10.017065 CUS FINITION CESSION RSION YWORDS	781 968	721 908	661 848	601 788	541 728	481 668	421 608	361 548	301 488	428
NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Ilssue Procurement: DCTD/DTP/Gazdar CDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Group at the Stanford Human Genome CNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	Homo sapiens Homo sapiens Homo sapiens Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1125) Strausberg,R. Direct Submission Submitted (05-NOV-2001) National Institutes of Health, Mammalian Submitted (05-NOV-2001) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	BC017065 Homo sapi 6b, decoy BC017065 BC017065 MGC.	CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813	GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGGGCGTGGCCAGGATGCCCGGGCTGGAG 780	CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGGGGGCTCACGGAGCTCCTGGGGGCGCAGGAC 720	CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC	GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600	GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540	CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480	TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAG	

Clone distribution: MGC clone distribution information can be found

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AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTTGGAGCAC 300
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134. .1036
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Sequence 1 from Patent W09946376.
AX017828 AX017828.1 GI:10042431
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VARQDISIKRLQRLLQALEAPEGWGPTPRAGRALQLKLRRITELLGAQDGALLVRL
LQALRVARMPGLERSVRERFLPVH"
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through the I.W.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 22 Row: d Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14790166.
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/codon_start=1
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/db_xref="LocusID:8771"
/db_xref="Laxon:9606"
/clone="MGC:958"
/closue_type="Lung, carcinoma, large cell
undifferentiated."
/clone_lib="NIH MGC_69"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
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                                                                                                   Location/Qualifiers
1. .1125
/organism="Homo sapiens"
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Receptor from the superfamily of tnt-receptors from the human lung
Patent: WO 9946376-A 1 16-SEP-1999;
BASF AG (DE); KROEGER BURKHARD (DE)
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 813; DB 6; L
Best Local Similarity 100.0%; Pred. No. 6.5e-125;
Matches 813; Conservative 0; Mismatches 0;
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
FEATURES
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Sequence 18
AR171895
AR171895.1
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                                                                                                                                                                Polynucleotide encoding TNFL1
Patent: US 6297367-A 18 02-OCT-2001;
Location/Qualifiers
1. 1347
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Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Caskey,C.T.
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Bai,C.
Direct Submission
Submitted (21-DEC-1999) WP26A-1000,

Merck Research Laboratories,

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(bases 1 to 1428)

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/product="KIAA108" protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 6 (3), 197-205 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3944) On May 9, 2002 this sequence version replaced gi:5689512.

Location/Qualifiers
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/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DN
fragments derived from two cDNA clones (1 - 834 was
derived from a RT-PCR product (Brain) and 835 - 4945 was
derived from hk02589)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
1182 CGCGCGCCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC 1241
                                                                                                                        GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGCGTGGCCAGGATGCCCGGGCTGGAG
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
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LKQRSSGSPAAGDPESSLCVEYEQEPVPARQRERGLLAALEHEGRAGSPGEEQAHSC
STLSLLSEK PAEEEPRGERKKI RLVSHPEEPVALQAQOTDAEHHKQKGELSQANFAT
FTQALQDY KGSDDFAALAACLGPLFAEDPKHLLQGFYQFVRPHHKQKDEESVCTQLT
FTQRCGYRPEHS I PRRQRAQPVLD PTGRTAPDPKLTVS TAAAQQLDPQEHLNQGRPHLS
RPPPTGDPGSHPQMGSCVPRACKQGDAVSAYLADARRALGSGCSQLLAALTAYKQ
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SGSPPHGPAASEMGEPHGRD I AGQQATGAPGGPLSAGCVQGCGAEDVVPFQCPACDF
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GRCQACMQRHLGASRMCPACHTASRKQGVMQVFMPEHKDHEGAGGAREVAAVPGVGA
GRCQACMQRHLGASRMCPACHTASRKQGVMQVFMPEHKDHEGAGGAREVAAVPGVGA
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                                                                        Matches 812;
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                                                                                                                                                                                           COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4775
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GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: o Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 14790166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC034349 1150 bp mRNA linear PRI 08-JU
Homo sapiens, tumor necrosis factor receptor superfamily, men
6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, i
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1150)
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                                                                                               Similarity
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                                                                        Conservative
                                                                                                                                                                                                                                      /protein_id="AAH34349.1"
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VAFODISIKRLQRLLQALEAPEGWGFTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
                                                                                                                                                                                              LQALRVARMPGLERSVRERFLPVH"
382 c 348 g 198
                                                                                                                                                                                                                                                                                                                                                                                                                                      member 6b, decoy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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/clone_lib="NCI_CGAP_Skn4"
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/db_xref="taxon:9606"
/clone="MGC:21079 IWAGE:4752507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV-SPORT6.ccdb"
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Pred. No. 1.2e-124;
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, R.G., Muzny, D.M.,
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                                                                     316 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTAGAGCGCTGCCGC 375
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196 GTGGCAGAAACACCCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGTGC 255
                                                                                                                                         AACCGIGCCIGCCGCIGCCGCACCGGCIICTICGCGCACGCIGGIITICIGCTIGGAGCAC 300
                                                                                                                                                                                                                                                                                                                                                                                             CCCCCCCCTTCCACCCTCAAGCTGCGTCGCGGCCTCACGGAGCTCCTGGGGGCGCACGGAC
                              256 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGAGCG
                                                                                                   GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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Search completed: January 6, 2003, 14:40:26 Job time : 2682 secs

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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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seq length: 2000000000
N Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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813
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	% Query Match Length DB	Length		ID	Description
1	813	100.0	813	20	AAZ25377	Human mFLINT #1 nu
N	813	100.0	813	21	AAA75999	DNA encoding a mat
ω	813	100.0	813	21	AAA88730	Human FAS ligand i
4	813	100.0	813	21	AAA51077	Mature human FLINT
Ŋ	813	100.0	813	22	AAD07380	Human mature fas 1
6	813	100.0	813	24	AAD27868	 Human mature FLINT
7	813	100.0	900	20	AAZ25375	Human FLINT #1 nuc
6	813	100.0	900	21	AAA53208	Human Fas ligand i
9	813	100.0	900	21	AAA51075	Human FLINT coding

Human soluble TNF	AAC63765	21	1859	5	533.4	45
DNA encoding a hum	AAX89503	20	899	٠		44
Human APO6 DNA. H	AAX23419	20	767	φ.	A	43
119	AAA53209	21	900	.9	28.	42
ovari	ABQ55057	24	1224	.80	•	41
hum	AAZ92404	21	1137	9	09.	40
FLINT	AAD27869	24	936	۰	09.	39
Human FLINT native	AAF77696	22	936		09.	38
	AAF84739	22	936	φ.	09.	37
	AAF84738	22	936	φ.	09.	36
Nucleotide sequenc	AAF89920	22	936	٩	09.	35
	AAD07385	22	936	٩	09.	34
Human FLINT coding	AAA51076	21	936	۰	09.	33
Human FAS ligand i	AAA88731	21	936	٩	09.	32
NT #2 nu	AAZ25376	20	936	φ.	11.	31
Human mature FLINT	AAA51078	21	825	۰	11.	30
Human mFLINT #2 nu	AAZ25378	20	825	. 6	-	29
	AAX76052	20	1462		813	28
M68 TNF receptor r	AAA53801	21	1428		813	27
Human soluble TNF	AAC63764	21	1347		813	26
Human tumour necro	AAX07226	20	1205	.0	813	25
Human colon cancer	AAH33171	22	1179		813	24
	AAZ09998	20	1168		813	23
Nucleotide sequenc	AAV07654	19	1164		813	22
	AAC91462	22	1114		813	21
Human PRO212 polyp	AAC84421	22	1114		813	20
PRO212	AAA77537	21	1114		813	19
pro	AAC58581	21	1114		813	18
nucl	AAC58367	21	1114		813	17
d ⁷ 1	AAX32744	20	1114		813	16
Human tumour necro	AAD33281	24	1077		813	15
Human tumour necro	AAA37772	21	1077		813	14
Human tumour necro	AAV39085	19	1077		813	13
M68 TNF receptor r	5380	21	g)		813	12
NTR3 nuc	27	22	1055	100.0	813	11
epto	AAX22300	20	0		813	10
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ALIGNMENTS

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17-DEC-1999
                          AAZ25377;
                                                     AAZ25377 standard; cDNA; 813
(first entry)
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Human mFLINT #1 nucleotide sequence.

Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; WO9950413-A2 Homo sapiens myocardial ischaemia; ss. growth; myelodysplastic syndrome; pancytopenic condition;

RRESULT 1
AAZ25371
ID AAZ2537
XX AAZ2537
XX AAZ2537
XX Huma
DE Huma
XX 30-MAR-1998; 20-MAY-1998; 09-SEP-1998; 17-DEC-1998; 18-DEC-1998; 22-DEC-1998; 30-MAR-1999; 07-OCT-1999 98US-0079856. 98US-0086074. 98US-0099643. 98US-0112577. 98US-0112703. 98US-0112933. 98US-0113407. 99WO-US06797

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AAA75999;
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with trombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder. Type I diabetes, cancer, cell damage or damage to an innocent bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that thave been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac mycoyte resulting from abnormal myocardial ischaemia. The present sequence
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                                                                                                                                                                                                                                                  Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCCACGCTGGTTTCTGCTTGGAGCAC
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                                                       Hale JE, Heuer JG;
Noblitt TW, Reidy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                    Bumol TF, Dou S, Glasebrook AL, Gould KE,
Hui KY, Kharitonenkov A, Mizrahi J, Na S,
Song HY, Wang J, Wu X, Zuckerman SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 813; D
100.0%; Pred. No. 5.1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Fig 3; 99pp; English.
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ELI
                                                                                                                                                                           WPI; 1999-591319/50
(ELIL ) LILLY & CO
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Matches 813; Conserv
                                                                                                                                                                                                             P-PSDB; AAZ42184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present sequence encodes a mature human FAS Ligand Inhibitory protein (FILNT): FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAS Ligand Inhibitory Protein analogs useful for treating abnormal apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease ulcerative colitis or Crohn's
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Witcher DR;
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                               GACACCCTGTGCACCAGCTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG
                                                                                                                    GAGTGTGAGCGTGCCGTCATCGACTTTGTGTGTTTCCAGGACATCTCCCATCAAGAGGCTG
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                                                                                                                                                                                                                                CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGCTCACGGAGCTCCTGGGGGGCGCAGGAC
                                                                                     GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTTCCAGGACATCTCCATCAAGAGGCTG
                                                                                                                                                                                                DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, FAS Ligand Inhibitory Protein, FLINT, analogue, apoptosis, tumour necrosis factor receptor; acute lung injury; pulmonary fib acute respiratory distress syndrome; ulcerative colitis, chronic obstructive pulmonary disease; Crohn's disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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99US-0140077.
99US-0140156.
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Newton CM, Noblitt TW,
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P-PSDB; AAB19334.
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21-JUN-1999;
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Best Local Sim
Matches 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 813 BP; 122 A; 298 C;
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                                                                                                                                 CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCCCAGGAC
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                  CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
                                                                                                                                                                         CAGCGGCTGCTGCAGGCCCTCGAGGCCCCCGGAGGGCTGGGGTCCGACACCAAGGGCCGGC
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Pred. No. 5.1e-145;
; Mismatches 0;
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813
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                                                                                                                     inhibitory protein FLINT mature protein (see AAB19705). FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, the reventing its interaction with FAS. This interaction is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis. The invention relates to novel FLINT analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence. Nucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT cDNA is used as a template for introducing the registrant FIINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, chronic obstructive pulmonary disease, pulmonary fibrosis, to inhibit T lymphocyte activation, and to facilitate organ
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04-AUG-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protease resistant FAS ligand inhibitory protein analogues resistant to in vivo or in vitro proteolysis at amino acid posit: of the mature protein, useful for treating autoimmune diseases
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Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNPR) superfamily member, which binds Fasl and LIGHT and prevents Fasl-Fas interaction. Mature FLINT (WFLINT) inhibits Fasl-Fas mediated apoptotic and pro-inflammatory activity. WFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting inchming ischemic injury during organ transplantation or for organ preservation during transplantation. MFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemocherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
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99WO-US30734
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                                                  98US-0113407
                                                                                                  99US-0172239
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Best Local Similarity 100.
Matches 813; Conservative
                                                                                                                                                     (ELIL ) LILLY & CO ELI
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                                                22-DEC-1998;
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07-DEC-1999;
07-DEC-1999;
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; 99US-0169381.
; 99US-0169412.
; 2000US-0191430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Human mature fas ligand inhibitory protein
(FLINT)"
/note= "CDS does not include start and stop codon"
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(FINT) CDNA. FLINT, a homologue of tumour necrosis factor receptor crocking conversion (TNPR), binds fas ligand (FASE) and thereby preventing the interaction of FasE with fas. FLINT comprising O-linked or N-linked CC oligosaccharides is useful for preventing or treating acute lung injury (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis, chronic obstructive pulmonary disease (POP) and pulmonary fibrosis (PP), CC chronic obstructive pulmonary disease (ARDS), ulcerative colitis, chronic obstructive pulmonary disease (ARDS), ulcerative colitis, to facilitate organ preservation for transplantation and to inhibit T CC lymphocyte activation. FLINT is useful for treating and/or preventing diseases such as rheumatoid arthritis, fibroproliferative lung disease, fibrotic lung disease, acute lung injury, human immunodeficiency virus (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-host disease, cutaneous inflammation, vascular leak syndrome, Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease, crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as poriasis, Down's syndrome, and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked oligosaccharides -
Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human mature fas ligand inhibitory protein (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor recepto
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δ 밁 Ś 밁 Ş 밁 Ş 밁 Ś 밁 Ś 밁 S Ś 밁 밁 망 Ś Matches Query Match Best Local : 361 301 301 421 361 181 181 121 121 61 61 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGTGC GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAG CCCCACCGCAACTGCACGGCCCTGGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCCAGAGCAGTGCCAG TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCCAGAGCAGTGCCAG AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGACGGGCTTGCCACGCCAC TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC GCCCAGTGCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCGAGACAGCCCCACGACG GCCCAGTGCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 813; Similarity Conservative 100.0%; Score 813; DB 22; 100.0%; Pred. No. 5.1e-145; 0; Mismatches 0 Indels <u>.</u> 480 540 480 420 420 360 300 240 60 60 540 360 240 180 0

GAGTGTGAGCGTCCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a new method of administering FLINT (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -
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                                                                                                         GGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780
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GAGTGTGAGCGTGCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCATCAGAGGCTG
                                         CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGCTCACGGAGCTCCTGGGGGCGCAGGAC
                                                                              CGCGCGCCTTGCAGCTGAAGCTGCGCGCGCTCACGGAGCTCCTGGGGGCGCAGGAC
                                                                                                                                                                                                                                                                                           FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis; organ failure; liver; kidney; panoreas; inflammatory disease; entropoli; sepsis; acute respiratory distress syndrome; acute lung injury; systemic inflammatory response syndrome; siRS; multiple organ dysfunction; MODS; human; gene; ds.
                              /product= "Mature FLINT protein"
/note= "Does not include start and stop codons"
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                                                                                                                                                            CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
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treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS)). The method minimises the pain and discomfort of injection methods. The present sequence is human
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100.0%; Pred. No. 5.1e-145;
ive 0; Mismatches 0;
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CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor CC superfamily, is used for treating acute liver failure, inflammation of CC with inflammation, hepaticis, abnormal apoptosis, a disorder associated CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia associated CC injury or disorder such as hypercoagulation (including use with CC thrombolytic or anti-thrombolytic agente), reperfusion associated injury CC or disorder, Type I diabetes, cancer, cell damage or damage to an CC innocent bystander tissue that is induced by a chemotherapeutic agent or CC therapeutic irradiation, treating haematopoietic progenitor cells that CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mplint is CC also used for promoting the growth or differentiation of a haematopoietic cresulting from abnormal myocardial ischaemia. The present sequence CC encodes human FLINT.
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                                                                                                     Query Match
Best Local &
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20-MAY-1998;
09-SEP-1998;
17-DEC-1998;
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                                                                                                   Sequence
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18-DEC-1998;
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             GTGGCAGAAACACCCACCTACCCCTGGCGGGACGGAGAGACAGGGGGAGCGGCTGGTGT
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GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC
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                                                  Conservative
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98US-0112703.
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98US-0113407.
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Zuckerman SH;
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Pred. No. 5.1e-145;
Mismatches 0;
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                                                                                                                                                                                          Fas ligand inhibitor; FLINT; apoptosis; autoimmune nation; infectious disease; ischaemia; Alzheimer's of son's disease; transplantation; ss
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FLINT, osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR; FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                      CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGCTCACGGAGCTCCTGGGGGCGCGAGGAC
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99WO-US06797.
99US-0172239.
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30-MAR-1999;
20-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the coding sequence of the human Fas ligand
inhibitor (FLINT). The FLINT protein is involved in cell-specific
conditions are used to treat inflammatory and autoimmune diseases
such as rheumatoid arthritis, inflammatory bowel disease,
the crown state of disease, diabetes, psoriasis and Graves' disease,
confections diseases such as HIV-induced lymphopenia, fulminant viral
thepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
conferation, ischaemia and reperfusion conditions including acute
conferation, ischaemia and reperfusion conditions including acute
and atherosclerosis, and Alzheimer's and parkinson's disease, brain
trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
multiple sclerosis. In addition, the gene and protein can be used to
prevent apoptosis following organ transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                   monkey Fas ligand inhibitor polypeptides, useful for treating mmatory or autoimmune disease such as rheumatoid arthritis, ious diseases such as chronic hepatitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACG
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ilarity 100.0%; Pred. No. 5.1e-145;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 88-91; 101pp; English.
/product= "FLINT"
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98US-0111580.
99US-0115069.
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Best Local Similarity
Matches 813; Conserv
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09-DEC-1998;
07-JAN-1999;
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factor receptor (TWFR) superfamily member, which binds Fast and LIGHT and

prevente Fast-Fas interaction. Mature FLINT (mFLINT) inhibits Fast-Fas

mediated apoptotic and pro-inflammatory activity. mFLINT is useful for

treating acute respiratory distress syndrome, treating or inhibiting

culcerative collitis, inhibiting ischemic injury during organ inhibiting

transplantation or for organ preservation during transplantation. mFLINT

can also be used to treat acute liver failure, inflammation of the liver,

abnormal (hepatocyte) apoptosis, sepsis, disorders associated with

inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,

damage to a cardiac mycoyte resulting from abnormal mycoardial ischaemia,

Type I diabetes, cancer, damage to an innocent bystander tissue induced

by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,

myelodysplastic syndromes and pancytopenic conditions.
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Best Local Similarity
Matches 813; Conserv
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DB; AAY96596.
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vative 0; Mismatches 0;
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Query Match Best Local Sim Matches 813;

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Mismatches

Indels Length

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903;

5.1e-145; DB 20; Sequence

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                        This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The protein is related to osteoprotegerin (OPG) and to tumour necrosis factor receptor (TNFR). Host cells transformed with a vector comprising the HUMAN NTR-1 nucleic acid are used for the recombinant expression of the protein. HUMAN NTR-1 proteins and antibodies immuno specific for the protein are useful for diagnosis and treatment of humans and animals, especially muscle disorders, as the receptor is involved in regulation of bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful for screening for novel binding agents, and cognate ligands, which may be used to treat disorders associated with HUMAN NTR-1 imbalance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human; tumour necrosis factor receptor; muscle disorder; bone mass; scr muscle metabolism; binding agent; cognate ligand; ss.
                                                                                                                                                                                                           Novel orphan human receptor polypeptide and nucleic acid - diagnostic reagents and for treatment of muscle disorders
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The present sequence encodes the tumour necrosis factor (TNF) receptor polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiency syndrome (AIDS), anemia, autoimmune diseases, cachexia, cancer, cerebral malaria, disbeties mellitus, disseminated intravascular coagulopathy, erythroid sick syndrome, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia, obesity, rejection of transplanted organs, rheumatoid arthritis, septic shock syndrome, stroke, adult respiratory distress syndrome (ARDS), tuberculosis, and a number of viral diseases. The NTR3 polypeptide is useful for identifying or developing new (ant) agonists of NTR3. It may be useful as mimunogen to which antibodies may be raised. NTR3 uncleic acid molecules may be useful as hybridisation probes in diagnostic assays to test, either qualitatively or quantitatively, for the presence of an NTR3. DNA or corresponding RNA in mammalian tissue or bodily fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tumor necrosis factor receptor, NTR3, useful for treating cancers, stroke, anemia, obesity, rheumatoid arthritis and transplantation rejection -
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                                                                              05-FEB-1999;
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The M68 protein is a member of a family of proteins which have croles in immune responses, cell death, cell proliferation and standard of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural conhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that m68 modulators of M68 will be useful in treatment of apoptosis-related diseases such as various forms of cancer and various bone disorders. M68 mucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxodema, autoimmune cliver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephritis, pulmonary fibrosis, heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21;
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Query Match 100.0%; Score 813; DB 21; Length Best Local Similarity 100.0%; Pred. No. 5.1e-145; Matches 813; Conservative 0; Mismatches 0; Indels Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

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atherosclerosis, aplastic anaemia, myelodisplastic syndromes, osteoporosis, Alzheimers disease, Parkinsons disease, stroke, myocardial infarction.

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                                                                                                                                                                                                                                                                                          Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
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P-PSDB; AAW63622.
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particularly of the immune system, substantially altered (whether increased or decreased) levels of TNRF-6 alpha and/or TNFR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR-6 alpha and TNFR-6 beta genes can also be detected. The TNFR-6 alpha and also claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
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                                                                                                                                                                                                                                                                                         Length 1077;
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                                                                                                                                                                                                                                      Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
                                                                                                                                                                                                                                                                                      100.0%; Score 813; DB 19;
100.0%; Pred. No. 5.1e-145;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                           813; Conservative
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alpha (TWFR-6alpha) of the invention. The TWFR-6alpha and TWFR-6beta DNA cand protein sequences can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate TWFR expression. The nucleic acids, polypeptides, antibodies, agonists and antagonists against them may be used for the treatment of a range of conditions such as cidisorders associated with neovascularisation (especially ocular neovascularisation) (such as solid tumours and malignancies (e.g. prostate cancer, breast cancer and colon cancer), diabetic retinopathy and pre-maturity macular degeneration, allergies, inflammation, thyroid associated opthalmopathy tissue/cell damage, wounds, microbial and parasitic infections, bone disease (e.g. osteoporosis), atheroselerosis, pain, cardiovascular disease (e.g. stroke), neurodegenerative disorders (e.g. Alzheimer's disease, immune caltommune diabetes, asthma, psoriasis, septic shock and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1999;
12-MAR-1999;
27-APR-1999;
30-APR-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocular neovascularisation; solid tumour; malignancy; prostate cancer; breast cancer; colon cancer; diabetic retinopathy; microbial infection; pre-maturity macular degeneration; allergy; inflammation; tissue damage; thyroid associated opthalmopathy; cell damage; parasitic infection; bone disease; osteoporosis; atherosclerosis; cardiovascular disease; neurodegenerative disorder; Alzheimer's disease; immune disorder; graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human tumour necrosis factor receptor proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g. Alzheimer's disease, osteoporosis and graft rejection -
                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                                                                                                                                                                                         sequence encodes the human tumour necrosis factor receptor 6
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DB; AAY90357.
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99US-0124092.
99US-0131279.
99US-0131964.
99US-0146371.
99US-0168235.
                                                                                                                                                                                                                                                                                                     332pp; English
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Query Match

Sequence

1077

B₽;

196 A; 360

C;

326

G; 195

0 other

100.0%;

Score 813;

DB Η.

21; Length 1077;

Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; th immune system-related disorder; inflammatory disease; immunosuppres bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;

01-JUL-2002

entry)

tumour

necrosis (first

factor

receptor (TNFR)-6alpha

CDNA

IMFR-6beta; therapy; immunosuppressive;

AAD33281

standard;

CDNA; 1077

ВP

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RESULT 19
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autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; crobn's disease; autoimmune encephalitis; allergy; graft versus host disease; GWHD; antiinflammatory; psoriasis; arthritis; neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human tumour necrosis factor receptor (TNFR)-
Galpha and 6beta protein and their corresponding nucleic acids. The
invention provides screening methods for identifying agonists and
antagonists of TNFR-6alpha and 6beta activity. The invention also
provides diagnostic and therapeutic methods for detecting and treating
immune system-related disorders. The method is useful for treating or
preventing an inflammatory disease or disorder selected from bowel
disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
disease or disorder selected from systemic lupus erythematorsus,
arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
and autoimmune encephalitis, graft versus host disease (GVHD), and an
allergy or asthma. The present sequence is human TNFR-6alpha cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecules comprising a polynucleotide encoding humar tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides useful for treating disease e.g. inflammatory and autoimmune disorders
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AW662363
BM756086
BM831338
AI718743
BM759026
BM831338
BEF001490
BF001490
BM738195
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BM833454
BM857727
AI857227
AI8572727
AI857727
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BM767088
BM767418
BM743072
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BG679499
BF339551
AW262121
BQ019285
BI838357
BE879166
AW471440
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Homo
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AW083241 XC07a04.X
AW262121 XG31d04.X
BQ019285 UI-H-DT1
B1838357 603083306
BE879166 601486906
AW471440 XW59906.X
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AW083915 K-EST0002
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source Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: n column: 15
High quality sequence stop: 758.
Location/Qualifiers

rce Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1118)
11 Homo:
12 Homo:
13 Homo:
14 Homo:
15 Homo:
16 Homo:
17 Homo:
18 Homo bp mRNA linear EST 04-OCT-2001 sapiens cDNA clone IMAGE:5176910 5', ьe

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73.1%;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="INAGE:5176910"
/clone="INAGE:5176910"
/clone="INAGE:5176910"
/clone="Most="DH10B"
/lab_host="DH10B"
/note="Grgan: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: Not!; Site_2: EcoRv (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; nale lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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larity 99.4%; Pred. No. 2.2e-113;
Conservative 0; Mismatches 0; Indels 4.
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BE878908 617 bp mRNA linear EST 20-OCT-2000 601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5', ä /db_xref="taxon:9606"
/clone="IMAGE:3894794"
/clone=lib="NIH_MGC_69"
/clone=lib="NIH_MGC_69"
/tissue type="large_cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies." Chordata, Craniata, Vertebrata, Buteleostomi, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 617)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999) þe 182 242 455 302 515 362 575 422 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9685 row: a column: 03
High quality sequence stop: 617. Gaps 62 3 CTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGA GGGCACCCCCAGCCAGAACACGCGAGCCAGCCGTGCCCCCCCAGGCACCTTCTCAGCCAG GGCACGGGCTTGCCACGCCACCCACAACCGTGCCGCTGCCGCACCGGCTTCTTCGC 123 GCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCC CAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTT 216 GGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGC GCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCC CAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCT CAGCTCCAGCTCAGAGCAGTGCCACCCCACCGCAACTGCACGGCCCTGGGCCTTGGCCCTT CAATGTGCCAGGCTCTTCCTCCCATGACACCTGTGCACCAGCTGCACTGGCTTCCCCCT CAATGTGCCAGGCTCTTCCTCCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCCCCT 1; Length 617; Indels ; 0 Score 594; DB 12; Pred. No. 1.3e-101; 0; Mismatches 66 1. .617 /organism="Homo sapiens" 203 g BE878908.1 GI:10327684 363 셤

635

CCAGGACATCTCCATCAAGAGGCTGCAGCGCTGCTGCTGCAGGCCCTCGAGGCCCCCGGAGGG

576

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RESULT 2 BE878908

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics (www.resgen.com).
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Program for Rat Gene Discovery and Mapping
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1 (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT/T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gen Discovery in the Visual System, supported by National Eye
                                                                                                                                                             /tissue_type="fetal eye"
/dev_gtage="fetal"
/lab_host="Dflow Life Technologies) (T1 phage resistant)"
/lab_host="Dflow Life Technologies) (T1 phage resistant)"
/note="Organ: eye, Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-EO1 is a normalized cDNA library containing the
following tissue(e): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
                                                                                                                                                                                                                                                                                                                                        /clone="UI-E-EO1-ajc-j-12-0-UI"
/clone_lib="UI-E-EO1"
                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                            mRNA sequence.
BE878006
BE878006.1 GI
EST.
                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 679)
11. MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                  /organism="Homo sapiens"
/db_xref="texon:9606"
/db_mundE:3891908"
/clone=lib="NHH MGC 69"
/tissue_type="large_cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="vogan: lung, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution. MGC clone distribution information can
found through the I.M.A.G.E. Consortium/Linn at:
http://image.llnl.gov
Plate: LinMAG77 row: h column: 21
High quality sequence stop: 672.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTGCCAGCCCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCAGTG
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100.0%; Pred. No. 1.9e-98;
ive 0; Mismatches 0;
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AGENCOURT 8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:62506915', mRNA sequence.
BQ687526

DEFINITION

ACCESSION VERSION

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4
Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
CONA Library Preparation: Rubin Laboratory

CONA Library Preparation: Rubin Laboratory

DNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 599.

Location/Qualifiers

Location/Qualifiers
                          Euteleostomi;
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REFERENCE
AUTHORS
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SOURCE
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1 (bases 1 to 572)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 3 row: E column: 03
High quality sequence stop: 572.
Location/Qualifiers
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Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
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21C Frontier Korean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kim YS
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/note="Organ: Stemach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and
                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Lymphoblast-like"
/cell_line="SNU-5"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Ascites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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VERSION KEYWORDS

BM480312 BM480312.1 EST.

GI:18529354

ACCESSION

SOURCE

human.

ORGANISM

Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

LOCUS DEFINITION RESULT 7 BM480312

BM480312 1203 bp AGENCOURT_6424187 NIH_MGC_67 Homo 5', mRNA sequence.

sapiens mRNA

CDNA linear E cDNA clone

EST 05-FEB-2002 MAGE:5491790

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                                                 GGGCCGCGCGCCTTGCAGCTGAAGCTGCGTC
                                                                                                                                                 GCTGCAGCGGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC
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GGGCCGCGGCCTTGCAGCTGAAGCTGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription
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99.5%;
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Pred. No. 1.3e-96;
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1037)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10610 row: k column: 04

High quality sequence stop: 762.
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85.9%;
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/db xref="taxon:9606"

/clone="IMAGE:5491790"

/clone=lib="NHH MGC 67"

/tissue type="retinoblastoma"

/lab_nost="DH10B (phage-resistant)"

/note="Organ: ey; Vector: pCMV-SPORT6, Site_1: Not1;

Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.

Average innert size 1.75 kb. Library constructed by Life

Technologies."
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                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information clone distribution: MGC Clone distribution information on the found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12112 row: n column: 15
High quality sequence start: 4
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High quality sequence stop: 560.

Location/Qualifiers

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Pred. No. 8.3e-92;
0; Mismatches 12; Indels 7;
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                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution inform
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                           Plate: LLAM9508 row: p column: High quality sequence stop: 701.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE:4186995"
/clone_1ib="NCI_CGAP_Brn64"
/clone_1ib="NCI_CGAP_Brn64"
/tlssue_type="DH10B (TI_phage-resistant)"
/lab_host="DH10B (TI_phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: N
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                         Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 692)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                            AW081241 692 bp mRNA linear EST 14-OCT-1999 xc07a04.x1 NCI CGAP Co21 Homo sapiens cDNA clone IMAGE:2583534 3' similar to TR:O95407 DECOY RECEPTOR 3. ;contains L1.b1 MER22 repetitive element ;, mRNA sequence.
                                                                                                                                                    repetitive
AW083241
Unpublished (1997)
                                                                                               Homo sapiens
                                                                                                                         AW083241.1
EST.
               Tumor
                                                                                                               human.
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              Gene Index
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Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 299 c 301 g 145 t
                                                                                                                                       GI:6038393
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87.8%;
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                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
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                            Anatomy
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Bock, M.D., Ph.D. ChNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Stee_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Library constructed by Library constructed by Library constructed by Library constructions."
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
similar to TR:095407 095407 DECOY RECEPTOR 3. ;contains TAR1.b1
TAR1 repetitive element ;, mRNA sequence.
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/clone="INAGE:752231"
/clone=lib="NCI_CGAP_Lu28"
/tissue_type="type="type" aquamous cell carcinomas"
/lab_host="DH108"
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Location/Qualifiers
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                                                                      AW262121.1 GI:6638937
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       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Tachnologies, Inc. cDNA Library Arrayed by: Christa Prange, The
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
T.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Seq primer: -40UP from gibc.
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /db xref="rawn: 94prens" / db xref="rawn: 94prens" / db xref="rawn: 94prens" / clone="INAGE:2583534" / clone="Inage:2583534" / clone="Inage:2583534" / clone="Inage:2583534" / lab_host="DH10B" / lab_host="DH10B" / lab_host="DH10B" / cloned unidirectionally. Primer: Oligan: colon, Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Nor1; Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI_CGAP_Col8. Library constructed by Life Technologies." 115 t 1 others
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Pred. No. 9.1e-81;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
     Contact: Robert Strausberg, Ph.D.
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Matches 510, Conservative
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TITLE
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Best Local Similarity
Matches 458; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQ019285 568 bp mRNA linear UI-H-DT1-awn-l-19-0-UI.sl NCI_CGAP_DT1 Homo sapiens IMAGE:5891874 3', mRNA sequence.
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Unpublished (1997)
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Seq primer: M13 FORWARD
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                TAG_LIB=UI-H-DT1
TAG_TISUE=lung tetatastic chondrosarcoma
TAG_TISUE=SUE tetatastic chondrosarcoma
TAG_SEQ=AACTGTTCGG"

170 c 187 g 105 t
                                                                                                                                                                                                                                                                                                                                                                                                                                used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5891874"
/clone_lib="NCI_CGAP_DT1"
/tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                              library is AACTGTTCGG.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                          Score 458; DB 14;
Pred. No. 3.6e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11559 row: 1 column: 02
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        97
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

224 c 171 g 95 t 1 others
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_aref="IMAGE:5222545"
/clone="IMAGE:922545"
/clone="ID="NIH_MGC_120"
                                                                                                                                                                                                                 'lab_host="DH10B"
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Query Match

Score 428.6;

DB 13;

Length 588;

Life

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xw59e06.xl NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2832322 3' similar to TR:055407 095407 DECOY RECEPTOR 3. ;contains TAR1.bl AW471440
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
Life Technologies catalog #: 11548-013
Lone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNi at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 387.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 540)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                  DB 12;
                                                                                                  Score 421.6; DB 1:
Pred. No. 2.3e-69;
       Average insert size 1.1 kb. Technologies."
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                                                                                                  51.9%;
98.7%;
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Best Local Similarity 98.7
Matches 446; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DcTD/DrPF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9670 row: I column: 01
High quality sequence stop: 546.
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/organism="Homo sapiens"
/branism="Homo sapiens"
/dbxref="tas:388296"
/clone="Inb="NIH MGC_69"
/tissue_type="large_cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung, Vector: pCMV-SPORT6, Site 1: Not!;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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              Pred. No. 1.1e
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/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ; pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: OTigo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2 6/ptodata/2

2: /cgn2 6/ptodata/2

3: /cgn2 6/ptodata/2

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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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(c) 1993 - 2003 Compugen Ltd.
                     US-08-794-796-1
US-09-286-529-18
US-09-286-529-7
US-09-286-529-7
US-08-997-918-47
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Sequence 1, Appli
Sequence 19, Appli
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Sequence 47, Appli
Sequence 41, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
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Sequence 14, Appl Sequence 14, Appl	1, 3 j	Patent No. 5395760 Sequence 12, Appl Sequence 12, Appl	Sequence 10, Appl Sequence 3, Appli	Sequence 1, Appli Sequence 11, Appl	Sequence 1, Appli Sequence 18, Appl	Sequence 3, Appli Sequence 22, Appli Sequence 1, Appli Sequence 5, Appli

ALIGNMENTS

Title:

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; TOPOLOGY: 1; MOLECULE TYPE: US-08-794-796-1 ; Sequence 1, Application ; Patent No. 5885800 ; GENERAL INFORMATION: APPLICANT: Emery, COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2. CURRENT APPLICATION DATA: APPLICATION UNWBER: US/08/794,796 FILING DATE: 04-FEB-1997 CLASSIFICATION UNWBER: PAPLICATION DATA: APPLICATION NUMBER: 34,344 REFERENCE/DOCKET NUMBER: 34,344 REGISTRATION INFORMATION: TELEPHONE: 610-270-5219 TELEPHONE: 610-270-5219 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline STREET: 709 Swedeland APPLICANT: Tan, KB APPLICANT: Truneh, Alem APPLICANT: Young, Peter TITLE OF INVENTION: Tunor Necrosis TITLE OF INVENTION: TR4 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear STREET: 709 Swedeland CITY: King of Prussia STATE: PA LENGTH: TELEFAX: 610-270-4026 COUNTRY: US ZIP: 19406 Application US/08794796 1164 base pairs USA John Beecham Corporation Road Related Receptor,

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Score 813; DB 2; Pred. No. 2.6e-154;

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APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNF; FILE REFERENCE: 1408.003/20130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529; CURRENT FILING DATE: 1999-04-05; SOFTWARE: FASELSEQ for Windows Version 3.0; SEQ ID NO 18
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Pred. No. 2.6e-154;
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Patent No. 6297367
GENERAL INFORMATION:
PAPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TWI
FILE REFERENCE: 1408.003/200130.439C1
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Matches 813; Conserv
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CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 1859
TYPE: DNA
ORGANISM: Homo sapien
US-09-286-529-19
                                                                                                                                                                           US-09-286-529-7; Sequence 7, Application US/09286529; Patent No. 6297367;
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APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 7
LENGTH: 459
TYPE: DNA
ORGANISM: human
S-09-286-529-7
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Pred. No. 1.9e-98;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/997,918
CURRENT FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 525
TENETE: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application Patent No. 6077689
                                                                                                                                                                                      Matches
                                                                                                                                                                                                 Query Match
Best Local
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Snavely, Marshall TITLE OF INVENTION: ENHANCED FILE REFERENCE: A-496
                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: fragment encoding amino acids 22-194 of human
                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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                        GTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACG
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                                                                                                                       CACCTAAATATCTTCATTATGATGAAGAAACTAGTCACCAGCTGCTGTGCGACAAATGTC
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Pred. No. 7.2e-18;
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TYPE: nucleic
STRANDEDNESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION: 12-DEC-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE: NOMBER: 08/577,788
FILING DATE: ROBERT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08974022
Sequence 1, Application US/08974022
Sequence 1, Colison Beat Sequence 1, Application Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palcana
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STRANDEDNESS: single
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Best Local Similarity
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US-08-974-022-1
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US-08-974-022-1
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Gaps
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Mismatches 225; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UMMER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORBEY/ABENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRACTERISTICS:
L'ENGTH: 2432 base pairs
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1840 Dehavilland Drive
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
                                                                                                                                                                                                                                                                                                                         APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
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                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Osteoprotegerin NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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LOCATION:
                                                                                                                                                                                                         ADDRESSEE: Amgen Inc.
STREET: One Amgen Center
CITY: Thousand Oaks
STATE: California
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Pred. No. 2.8e-14;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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271
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-974-186-1
US-08-974-186
Sequence 1, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
APPLICANT: Lacey, David Lacey, Ming-Shi
APPLICANT: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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52.3%; Pred. No. 2.8e-14;
tive 0; Mismatches 225; Indels
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Patent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
NUMBER OF SEQUENCES: S3
CORRESPONDENCE AMGEN INC.
                                      US/08/974,186
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1840 Dehavilland Drive
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           NAME: Winter, Robert B.
RRPERENCE/SDOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52.3
Matches 247; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubbach
LENGTH: 2432 Dan-
TYPE: nucleic acid
TYPE: single
                                 APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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, LOCATION:
US-08-974-186-1
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US-08-795-446B-1
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271 TICGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATT 330
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                                                                                                                                                                                                                    US/08/795,446B
                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446
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US-08-706-945D-123
Sequence 123, Application US/08706945D
Parent No. 6368027
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Winter, Robert B.
REPERBUG/DOCKET NUMBER: J
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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California
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                                           91320-1789
                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
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; LOCATION:
US-08-795-446B-1
                    COUNTRY:
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US-08-974-022-3
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Best Local Similarity
Matches 247; Conserv
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SEQ ID NO 123
LENGTH: 2432
                                                                                                                                                                  Sequence 3, Application US/08974022 Patent No. 6015938
                                            GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
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CURRENT APPLICATION UNMEER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
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APPLICANT: Chang, Ming-Shi
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NAME/KEY: CDS
LOCATION: (124)..(1326)
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                            CORRESPONDENCE ADDRESS:
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Calzone, Frank
1840 Dehavilland
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nilarity 52.3%;
Conservative
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Pred. No. 2.8e-14;
0; Mismatches 225
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Best Local Similarity
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NAME/KEY:
LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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LENGTH: 1324 base pair
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APPLICATION NUMBER:
                               451
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603 CTGCTAATTCAGAAAGGAAATGCAACATGACAACGTGTGTTCCCGGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 91320-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                GGTGAGACTTCATCGAAAGCACCCTGTATAAAAACACACGAACTGCAGCACATTTGGCCCTC
                                                                                               GCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTG
                                                                                                                              CAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTCTCA
                                                                                                                                                               GCCCCGGGCACCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCA
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Pred. No. 5.5e-14;
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RESULT 13 US-08-795-445A-3

Sequence 3, Application US/08795445A Patent No. 6284485 GENERAL INFORMATION:

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91 CGGCCGTGCCGCCGAGACAGCCCCACGAGGAGGCCCGTGTCCACCGCGCGCACTACACG 150
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603 CTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACA 654
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.6%; Score 110.4; DB 4;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226;
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacy, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
VUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                       STREET: One Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                                    ; Sequence 3, Application US/08795447A; Patent No. 6284728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1324 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
US-08-795-447A-3
                                                                                                       RESULT 14
US-08-795-447A-3
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                                                                                                                                                                                                         STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
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13.6%; Score 110.4; DB 4;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226;
     APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UNDBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                         E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISCICS:
LENGTH: 1324 base pairs
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STRANDEDNESS: single
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US-08-974-186-3
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US-08-974-186-3
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 15 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                       183
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211 GAGGAGGCACGGGCTTGCCACGCCACCACACCCACAGCCTGCCCTGCCGCCACCGCACCGGCTTC 270
                                                      303
                                                                                    151
                                                                                                                       243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 CTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACA 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
COINTED. YOU
                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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90..1292
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                      GCCCTCAATGTGCCAGGCTCTTCCCCATGACACCCTGTGCACCACCAGCTGCA
CTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACA
                                                                 GGTGAGACTTCATCGAAAGCACCCTGTATAAAACACACGAACTGCAGCACATTTGGCCTC
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Search completed: January 6, 2003, 15:14:31 Job time : 59 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                    Database
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                                                                                                                                                                                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Listing first 45 summaries
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/ Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_Seq:*
/ Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq:*
/ Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq:*
/ Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_seq:*
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6062.518 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8.8	0.8	12.2	12.2	245.2	15.2	387	387.4	92.2	459	473.4	73.4	5.4	3.4	9.4	813	813	813	813	Score
26.9	27.2	29.8	29.8	30.2	30.2	47.6	47.7	48.2	56.5	58.2	58.2	63.4	65.6	99.6	100.0	100.0	100.0	100.0	Query
226	499	283	283	271	271	1796	1667	1550	459	491	491	903	1859	1137	1347	1114	1114	1077	Query Match Length
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
US-09-896-096A-9	US-09-935-727-17	US-09-894-924-10	US-09-896-096A-10	US-09-894-924-5	US-09-896-096A-5	US-09-935-727-28	US-09-935-727-3	US-09-935-727-33	US-09-877-156-7	US-09-894-924-3	US-09-896-096A-3	US-09-935-727-32	US-09-877-156-19	US-09-840-795-1	US-09-877-156-18	US-09-894-924-2	US-09-896-096A-2	US-09-935-727-1	ID
9	Sequence 17, Appl	Sequence 10, Appl	Sequence 10, App.	Sequence 5, Appl:	Sequence 5, Appl:	Sequence 28, App	Sequence 3, Appl	Sequence 33, App	Sequence 7, Appl	Sequence 3, Appl:	Sequence 3, Appl	Sequence 32, App.	Sequence 19, App	Sequence 1, Appl	Sequence 18, App.	Sequence 2, Appl	Sequence 2, Appl	Sequence 1, Appl	Description

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US-09-062-113-87	US-09-062-113-86	-062-113	US-09-062-113-84	-113	1	US-10-105-934-3	-113	US-09-062-113-100	-113	US-09-062-113-95	-113	-113	US-09-062-113-101	US-09-062-113-96	-09-062	US-09-062-113-102	US-09-894-924-7	US-09-896-096A-7	US-09-935-727-18	US-09-292-758-141	US-09-894-924-8	US-09-896-096A-8	US-09-894-924-6	US-09-896-096A-6	
					Sequence 6	Sequence :		Sequence 1								Sequence 1	Sequence 7	Sequence 7	Sequence 1	Sequence 141	Sequence 8	Sequence 8	Sequence 6	Sequence 6	
-	86, Appl	-	-	83, Appl	6, Appli	3, Appli	94, Appl	0	-	95, Appl	-	`_	ŗ	-	•	102, App	7, Appli	7, Appli	18, Appl	•	`	`	•	•	

ALIGNMENTS

RESULT 1 US-09-935-727-1

; PRIOR FILING DATE: 1997-0; NUMBER OF SEQ ID NOS: 42; SOFTWARE: PatentIn Ver. 2; SEQ ID NO 1; LENGTH: 1077 PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILLING DATE: 1999-04-27
PRIOR PELICATION NUMBER: 60/124,092
PRIOR FILLING DATE: 1999-03-12
PRIOR PELICATION NUMBER: 60/121,774
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILLING DATE: 1999-03-04
PRIOR PELICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR APPLICATION NUMBER: 60/035,496 Sequence 1, Application US/09935727 Patent No. US20020150583A1 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931 PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131 FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: 60/131,964 PRIOR FILING DATE: 1999-04-30 PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01 TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta APPLICANT: Human Genome Sciences, Inc. PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 1999-08-02 PRIOR FILING DATE: 2000-11-21 TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: CDS APPLICATION NUMBER: 60/146,371 1997-01-14

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APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: TOY, MARGARET A
APPLICANT: TOY, MARGARET A
APPLICANT: TOY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A THER Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
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ive 0; Mismatches 0;
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Sequence 2, Application US/09896096A
Patent No. US20020061559A1
GENERAL INPORMATION:
                                                                                                             Best Local Similarity 100.
Matches 813; Conservative
               LOCATION: (25)..(924)
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US-09-935-727-1
                                                                                         Query Match
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  Length 1114;
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Query Match
100.0%; Score 813; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0;
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APPLICANT: ASHKENAZI, AVI J APPLICANT: BOGTSTEN, DAVID APPLICANT: DODGE, KELLY H APPLICANT: GURNEY, AUSTIN L.

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APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: DODGE, KELLY H.
APPLICANT: KIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
FILE OF INVENTION: DOR3 POLYPEPTIDE, APPLICANT: WOOD, WILLIAM I.
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 2
LENGTH: 1114
TYPE: DNA
ORGANISM: HOMO Sapiens
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Patent No. US20020065210A1
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 813; Conserv
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NAME/KEY: Unsure
LOCATION: 1090
OTHER INFORMATION: Unknown
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1347
TYPE: DNA
CORGANIZAM: Homo sapien
US-09-877-156-18
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                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-66-08
                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                               Best Local Similarity Matches 813; Conserv
                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
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                                                                                                                                                                  100.0%; Score 813; DB 10; ilarity 100.0%; Pred. No. 8e-162; Conservative 0; Mismatches 0;
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                                               585 TACTGCAACGTCCTCTGCGGGGAGCGTGAAGGAGGAGGCACGACGACCACCCCCCC
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Patent No. US20020143147A1

GENERAL INFORMATION

APPLICANT: Mattson, Jeanine D.

APPLICANT: Bates, Blizabeth Esther Mary

APPLICANT: Bates, Blizabeth Esther Mary

APPLICANT: Bates, Blizabeth Sther Mary

APPLICANT: Bates, Blizabeth Sther Mary

APPLICANT: Bates, Blizabeth Sther Mary

APPLICANT: Lebecque, Serge J.E.

TITLE OF INVENTION: Mammalian Genes; Related Reagents

FILE REFERENCE: SP0818K

CURRENT APPLICATION NUMBER: US/09/840,795

CURRENT FILING DATE: 1099-07-12

PRIOR APPLICATION NUMBER: 09/351,777

PRIOR APPLICATION NUMBER: 09/351,777

PRIOR APPLICATION NUMBER: 1999-07-12

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 1

LENGTH 1137
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LOCATION: (99)..(998)
NAME/KEY: misc_feature
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Pred. No. 4.4e-161;
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US-09-877-156-19
; Sequence 19, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
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Matches 810; Conservative
LOCATION: (367)
OTHER INFORMATION: W;
NAME/KEY: mat_peptide
LOCATION: (132)..(998)
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US-09-840-795-1
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                                                                                                                                     Sequence 32, Application US/09935727 Patent No. US20020150583A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 537; Conserv
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LENGTH: 1859
TYPE: DNA
ORGANISM: Homo sapien
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NEW MEMBERS OF TWF AND FILE REFERENCE: 1408.003/200130.439C1 CURRENT EPILLORIUN NUMBER: US/09/877,156 CURRENT FILING DATE: 2001-06-08 PRIOR APPLICATION NUMBER: US/09/286,529 PRIOR FILING DATE: 1998-04-05 NUMBER OF SEQ ID NOS: 25 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 2.6e-103;
0; Mismatches 6;
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PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR PRIOR PRION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 903
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Best Local S
Matches 627
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ORGANISM: Artificial
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628
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APPLICATION NUMBER: 60/131,964
FILING DATE: 1999-04-30
APPLICATION NUMBER: 60/131,270
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FILING DATE: 1999-12-01
APPLICATION NUMBER: 60/146,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/121,774
FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/227,598
FILING DATE: 2000-08-25
APPLICATION NUMBER: 09/518,931
FILING DATE: 2000-03-03
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GAGTGCGAACGCGCTGTGATCGACTTTGTGGCCTTCCAGGATATCTCTATCAAAAGGCTG
                   GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
                                                             GATACTCTGTGTACAAGCTGTACTGGCTTTCCTCTCTCTACCCGCGTGCCTGGCGCTGAA
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Pred. No. 1.4e-99;
0; Mismatches 186
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161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGGAGGAGGAGCAC 220
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CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 240
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                                                                     TCCAGCTCAGAGCAGTGCCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGGCCTTCAAT
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                                             CCCCCAGCCAGAACACGCAGTGCC-AGCCGTGCCCCCAAGGCACCTTCTCAGCCAGCAGC
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APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT APPLICATION 1001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 473.4; DB 10;
98.8%; Pred. No. 7.6e-91;
iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR PLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
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OTHER INFORMATION: Unknown organism
NAME/KEY: unsure
LOCATION: 62, 73, 86, 98
OTHER INFORMATION: unknown base
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; Patent No. US20020065210Al
; GENERAL INFORMATION:
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APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: IAWRENCE, DAVID A.
APPLICANT: BOY, WARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
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es 485; Conservative
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                                                                747
                                                                                                                                                                                                                                    101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
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APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
ITILE OF INVENTION: DGR3 POLYPEPTIGE, A TNFR Homolog
TITLE REPERENCE: PI134R2 REVISED
CURRENT APPLICATION NUMBER: US 09/896,096A
CURRENT FILING DATE: 1990-09-18
PRIOR FILING DATE: 1990-09-18
PRIOR FILING DATE: 1990-09-18
PRIOR FILING DATE: 1990-09-18
PRIOR PILING DATE: 1990-09-18
PRIOR FILING DATE: 1990-09-18
PRIOR PILING DATE: 1990-09-18
PRIOR PILING DATE: 1990-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR PILING DATE: 1990-07-30
NUMBER: OF SEQ ID NOS: 18
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ilarity 98.8%; Pred. No. 7.6e-91;
Conservative 0; Mismatches 5;
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LOCATION: 62, 73, 86, 98
COTHER INFORMATION: unknown base
US-09-896-096A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: LAW, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: PITTI, ROBERT
APPLICANT: ROWA, MARGARET A
APPLICANT: WOOD, WILLIAM I.
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ORGANISM: Unknown
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LENGTH: 491
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Best Local 9
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Matches
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Sequence 7, Application US/09877156
Patent No. US20020055625A1

GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
ITILE OF INVENTION: NEW MEMBERS OF THE AND THE
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR APPLICATION NUMBER: US 09/286,529
INTHEER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7
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GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAGG
                                               TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCCTGGCCCTCAATGTGCCA
                                                                                                            TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGGCGTGATTGCCCCCGGGCACCCCC
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                             TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCCTCGATGTGCCA
                                                                                            TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC
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US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
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PRIOR FILLING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILLING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/168,235
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SOFTWARE: PatentIn Ver.
SEQ ID NO 33
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
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CURRENT FILING DATE: 2001-08-24
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1550
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APPLICATION NUMBER: 60/131,270
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APPLICATION NUMBER: 60/146,371
TGTGGCCCGTGTCCACCGCCCCCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
                                                                                                                                              GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCAGAGACAGCCCCCACGACG 120
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                                     TGTGGTCCATGTCCACCAAGACATTACACTCAATTTTGGAACTACCTGGAAAGATGTAGA 917
                                                                                                                     GCTCAATGTCCACCAGGTACTTTTGTTCAAAGACCATGTAGAAGAGATTCTCCAACTACT 857
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Pred. No. 8.6e-74;
0; Mismatches 263;
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REPERENCE: PF454P2
CURRENT APPLICATION WHRER: US/09/935,727
CURRENT APPLICATION WHRER: 00/303,224
PRIOR APPLICATION WHRER: 60/303,224
PRIOR APPLICATION WHRER: 60/252,131
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-00-25
PRIOR FILING DATE: 2000-00-25
PRIOR FILING DATE: 2000-00-25
PRIOR APPLICATION WHRER: 60/168,235
PRIOR APPLICATION WHRER: 60/146,31
PRIOR APPLICATION WHRER: 60/146,31
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION WHRER: 60/131,270
PRIOR APPLICATION WHRER: 60/131,270
PRIOR APPLICATION WHRER: 60/131,270
PRIOR APPLICATION WHRER: 60/124,092
PRIOR APPLICATION WHRER: 60/124,092
PRIOR APPLICATION WHRER: 60/124,774
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                                                                                978 AACAGAGCTTGTAGATGTAGAACTGGTTTTTTTTTGCTCATGCTGGTTTTTGTTTTGGAACAT 1037
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US-09-935-727-3
Sequence 3, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   Score 387.4; DB 10; Length 1667;
Pred. No. 8.8e-73;
0; Mismatches 1; Indels 136;
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 3
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79.68;
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Best Local Similarity 79.6
Matches 534; Conservative
                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (73)..(582)
US-09-935-727-3
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US-09-935-727-28
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PRIOR FILLING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILLING DATE: 1999-04-30
PRIOR FILLING DATE: 1999-04-27
PRIOR PRIOR PRIOR DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILLING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR APPLICATION NUMBER: 60/035,496
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PRIOR FILING DATE: 2000-11-21
PRIOR PEDLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
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Best Local Similarity
Matches 533; Conserv
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SOFTWARE: Patentin Ver
SEQ ID NO 28
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: intron
LOCATION: 425-560
NAME/KEY: intron
LOCATION: 756-1512
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CURRENT FILING DATE: 2001-08-24
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors
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                                                                 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCCG-----
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                                      GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 447
                                                                                                                         AACCGTGCCTGCCGCACCGCACCGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
                                                                                                                                                      AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
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79.4%;
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Pred. No. 1.1e-72;
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APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Unknown organism;
; NAME/KEY: unsure
; LOCATION: 42, 62, 73, 86, 98, 106, :
; OTHER INFORMATION: unknown base
US-09-896-096A-5
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Best Local Sim
Matches 250;
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                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 271
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                   161
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 221
                                                                                                                            101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 CCCTGAGCTAGGACACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCC
                                  19
                                                                                                        <u>بــ</u>
                                                      ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGGCGTGAGGAGGAGGAGCAC 220
GGGCTTGCCACGCCACCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG
                                ANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCCNTGAGGAGGAGGCAN 120
                                                                                                        GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACGCAGTTCTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTACCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTACCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCTCTTCCCCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGAGCAGTGCCAGCCCCACCGCCAACTGCACGGCCCTGGGCCCTCGACCCCAATGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCCTGGGCCCTCAATGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCCCAGGAGTGGTGGCCAGGTGTGGCAGGGTCAGGTTGCTGGTCCCAGCCTTGCA
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIM, KYUNG JIN
LAWRENCE, DAVID A.
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                73, 86, 98, 106, 120, 122, 153, 167, 184, 220, unknown base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758
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                                                                                                                                                                                         30.2%;
                                                                                                                                                                          0
                                                                                                                                                                        Score 245.2; DB 10;
Pred. No. 3.8e-43;
0; Mismatches 21;
                                                                                                                                                                                                             DB 10;
                                                                                                                                                                            Indels
                                                                                                                                                                                                             Length
                                                                                                                                                                                                             271;
                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                          Gaps
 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
121 GNGCTTGCCACGCCACCCACAACCGCGCTGCNGCTGCAGCACCGGNTTCTTCGCGCACG 180
                                                                                                  181 CTGNTTTCTGCTTGGAGCACGCATCGTGTCCCCCTGGTGNCGGCGTGATTGCNCCGGGCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCAC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCTTGCCACGCCACACACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG 280
                                                                         281 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 | GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACGCGGTTCTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Unknown organism

NAME/KEY: unsure

LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

COTHER INFORMATION: unknown base

US-09-894-924-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.2%; Score 245.2; DB 10; Length 271; 92.3%; Pred. No. 3.8e-43; Live 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANI JAPLICANT: ANI JAPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: DODGE, KELLY H.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: TUMAS, DAVIELE B.
APPLICANT: TUMAS, DAVIELE B.
APPLICANT: TUMAS, DAVIELE B.
APPLICANT: ROY, WARGARET A.
APPLICANT: NOOD, WILLIAM I.
TITLE OF INVENTION DCR3 POLYPEPTION OF SEVISED,
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271
                                                                                                                                                                    341 CCCCCAGCCAGAACACGCAGTGCCAGCCGTG 371
                                                                                                                                                                                                            241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCAGCCAGACACGCAGTGCCAGCCGTG 371
                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09894924
Patent No. US20020065210Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.33
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                             RESULT 15
US-09-894-924-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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Search completed: January 6, 2003, 16:08:07 Job time : 63 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09936024/runat_06012003_111607_12130/app_query.fasta_1.455
-Q=/cgn2_1/USPTO_spool/US09936024/runat_06012003_111607_12130/app_query.fasta_1.455
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=US09936024 @CGN 1 2425 @runat_06012003 111607_12130 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on:
                                                                                                                                                                                                                                                                                                                                   GenEmbl:*
1: gb ba:*
2: gb htg:*
3: gb om:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb pat:*
7: gb pt:*
9b pr:*
1: gb pr:*
1: gb ro:*
1: gb ro:*
1: gb ro:*
1: gb sts:*
1: gb sts:*
1: gb min:*
1: gb min
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
   2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                             em_mu:*
em_on:*
em_or:*
em_ov:*
em_pat:*
em_ph:*
em_ph:*
em_ro:*
em_un:*
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Ygapext
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2714.926 Million cell updates/sec
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_mus:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_prod:*
36: em_htg_wrt:*
37: em_htg_vrt:*
39: em_htg_onus:*
41: em_htgo_mus:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44		42	41	40	39	38	37	36	35	34	ω w	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	Ų	4	ω	2	1		No.	Result
N	24.	24.	25.		25.	433	436.5	.0	440.5	440.5		440.5	0	440.5	40.	440.5	486.5	499.5		287.	1287.5	1339	47	47	47	1476	4	1476	49	9	49	49	49	ø,	9	49	1491	9	1491	φ	1491	1491	1491	4		Score	
28.5	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•	•	33.5	•	4	4	•	99.0	•	•		99.0		00.	00.		00.	0	8	0	8	8	8					100.0	100.0		Match	Onerv
32	N	N	w	2432	ω	525	1356	2139	1719	1356	U	ហ	1355	0	1206	1156	1116	1148	459	50	4	1859	936	936	936	936	936	936	76	94	1428	ω	1168	5	12	1	11	H	5	2	0	\vdash	813		; ;	Length	
10	σ	თ	10	σ	σ	σ	σ	σ	9	9	σ	σ	σ	9	σ	φ	თ	տ	Φ	9	9	σ	σ	σ	σ	σ	9	ი	9	9	9	σ	σ,	9 1	9	9	σ	σ	თ	9	9	თ	σ	6		В	
w	558	AR168729 .	RNU94330	558	AR168728	913	AX076608	AX202074	BC030155	HSU94332	AX333682	AR205589	6873	214	E15271	AF134187	AF401631	OMY315137	AR171887	HSJ583P15	AF217796	AR171896	AX375171	AX167230	AX119836	AX098029	AX097545	AX093178	HSM802484	2	AF217793	AR171895	782	BC034349	BC017065	AF104419	56	5537	8286	AF217794	3424	516	AX167223	AX119833		ID	
3	88	68729	4330 Rattus	05587	68728	9131 S	ß	2074 Segue	Homo	`		05589	68730 Sequi	AB002146 Homo sapi	71 Human	87	AF401631 Oncorhync	15137	87	5 Humai	17796	896 S	5171 S	67230 S	9836 S	8029 S	7545 S	3178 Seque	57435	029011 Homo	7793 Homo	71895 S	7828 Segue	9 Homo	017065	4419 Homo	56645 S	55373 Se	82868 Seguence	17794 Homo sap	34240 Homo sa	75169 Sequenc	3 Sequence	119833 Sequen		Description	

ALIGNMENTS

	KEYWORDS SOURCE SOURCE Home sapiens CRGANISM Home sapiens ELKAIYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home. REFERENCE 1 (bases 1 to 813) AUTHORS Lu,J. and Witcher,D.R. TITLE Improving stability of flint through o-linked glycosylation JOURNAL Patent: WO 0142463-A 2 14-JUN-2001; ELI LILLY AND COMPANY (US) FRATURES 1. all Location/Qualifiers Source //organism="Home sapiens" /db_xref="taxon:9606" PARSE COUNT 122 a 298 c 267 g 126 t	ent No.: Si Scal Aatc	Qy 1 ValalaGluThrProThrTyrProTrpArgAspalaGluThrGlyGluArgLeuValCys 20	Qy 41 CysGlyProCysProbroArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60 ll	Qy 81 AsnArgAlaCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100 Db 241 AACCGTGCCGCTGCCGCACCCGCTTCTTCGCGACGCTGCTTTTGCAGCAC 300 Qy 101 AlaSerCysProProGlyAlaGlyValIHalaProGlyThrProSerGlnAsnThrGln 120 Db 301 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCAGAACACGCAG 360 Qy 121 CysGlnProCysProFroGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
AX119833 LOCUS DEFINITION Sequence 2 from Patent W00128582. AX119833 AX119832 AX119833 AX119833 AX119833 AX119833 AX119833 AX119833 AX119832 AX119833 AX119833 AX119833 AX119833 AX119833 AX119833 AX119832 AX119833 AX11983 AX119833 AX119833 AX119833 AX119833 AX11983 AX11983 AX11983 AX11983 AX11983 AX1	Alignment Scores: Pred. No.: Score: Score: 1491.00 Matches: Conservative: Best Local Similarity: 100.00\$ Minantches: Conservative: Guery Match: 6 Gaps: 0 05-936-024-1 (1-271) x AX119833 (1-813) QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 1 GTGGCAGAAACACCCCACCTGGCGGGACGCAGAGACGGCGTGTGC 60 OX 21 AlaGluCysProProGlyThrPhyProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 22 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 23 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 24 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 25 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX 26 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys OX AlaGluThrProThrTyrP	61 GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCCACGCGCGCG	OY 81 ASNAYGAIACYSARGCYSARGTPHYGIYPhePheAlaHisAlaGlyPheCysLeuGluHis 100 241 AACCGTGCCTGCCGCACCGGCACCGCACGCACGCTGGTTTCTGCTTGGAGCAC 300 OY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120 Db 301 GCATCGTGTCCCACCTGGTGCCGGCGTGTTTGCCCCGGGCACCCCCAGCAGAACACGCAG 360	Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerGluGlnCysGln 140 bb 361 TGCCAGCCGTGCCCCCCAGGCACTTCTCAGCCAGCTCCAGACTCCAGAGCAGTGCCAG 420 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160 Db 421 CCCCACCGCAACTGCACGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480	Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180 Db 481 GACACCTGTGCACCAGCTGCCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540 Qy 181 GluCysGluArgAlaVallleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200 Db 541 GAGTGTGAGCGTGCCGTCATCGAGGACTTCCAGGACATCTCCATCAAGAGGCTG 600 Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220

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Direct Submission
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Submitted (10-MAR-1999) Micro/Immunol, Indiana Barnhill Drive, Indianapolis, IN 46202, USA Location/Qualifiers
1. .903
                                                                                                                                                                        Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Ebner,R., A newly identified member of tumor necrosis superfamily (TR6) suppresses LIGHT-mediated J. Biol. Chem. 274 (20), 13733-13736 (1999)
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SSSSSEQCQPHRNCTALGALEANVPGSSSHDTLCTSCTGFPLGTRVPGAECGRAVIDF
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Matches:
Conservative:
Mismatches:
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/ Januarm="Homo sapiens"
/db xref="taxon:9606"
/cell_type="T lymphocyte"
/tissue_type="blood"
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Homo sapiens M68E mRNA, alternatively spliced, complete cds.
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/cell_type="adenocarcinoma"

/tissue_type="pancreas"
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ince="Thrps; decoy receptor; DCR3; alternatively spliced"

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1 (Dassel to 1048)
Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
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ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
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Sequence 1
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         Ntr3, a member of the tnf-receptor supergene family Patent: WO 0110908-A 1 15-FEB-2001;
                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly
                                                                GAGTGTGAGCGTGATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp

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TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 1114)

Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,

Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,

Tumas,D., Watanabe,C.K. and Wood,W.I.

Compositions and methods for the treatment of immune related
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Genentech, Inc. (US)
Location/Qualifiers
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                                                                                                                               Sequence 3 from Patent WO0073452.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bäses 1 to 1114)
Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
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Sequence 1 from Patent W00075316.
AX056645 GI:12309639
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Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
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Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C., Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T., Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L., Goddard,A.D., Botstein,D. and Ashkenazi,A.

Genomic amplification of a decoy receptor for Fas ligand in lunc
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (04-NOV-1998) Molecular Oncology, Genentech,
San Francisco, CA 94080, USA
Location/Qualifiers
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VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
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VARQDISTRRLQRLLQALLANPPGSSSHDTLCTSCTGFPLSTRVPGAEECRRAVIDF
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Matches:
Conservative:
Mismatches:
Indels:
note="Vector: pCMV-SPORT6"
                                                                       member 6b, decoy"
/protein_id="AAH17065.1"
/db_xref="GI:16877638"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds. BC017065 BC017065.1 GI:16877637
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
by Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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Submitted (05-MOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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 CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT
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/db_xref="taxon:9606"
/clone="MGC:9587 IMAGE:3886635"
/tissue_type="Lung, carcinoma, large cell
undifferentiated."
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Contact: MGC help desk
Cantact: Gapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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/lab_host="DH10B"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1479016
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Submitted (02-JUL-2002) National Institutes of Health, Mammalian Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC034349
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Yoon, V.S., Kowie, C.R., Lawrence, S., Martin, R.G.,
Richards, S., Gibbs, R.A.
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Center code: BCM-HGSC
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/db_xref="C1:21706465"
/db_xref="LocusID:8771"
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/lab_host="DH10B"
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/clone="MGC:21079 IMAGE:4752507"
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Polynucleotide encoding TNPL1
Patent: US 6297367-A 18 02-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                     Sequence 18 from patent US 6297367.
AR171895.1 GI:17910845
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/ Dece="unnamed protein product"
/ Anote="unnamed protein product"
/ codon start="I | 10042432"
/ translation="WRALEGFGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
/ translation="WRALEGFGESSLLCCPPRHYTOFRNYLERCRYCNVLCGRREEBA
RACHATHNRACNETGFRAMAGPCLEHASCPFGAAVIAFGTPSQNTQCQPCPFGTA
RACHATHNRACNETGFFAMAGPCLEHASCPFGAAVIAFGTPSQNTQCQPCPFGTSA
SSSSSEQCOPHRNCTALGLANVPGSSSHDTLCTSCTGFPLSTRVPGAEBCERAVIDF
VARQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
LQALRVARWEGLERSVRERFLVH"

192 c 371 g 211 t
         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1168)
Kroeger, B.
Receptor from the superfamily of tnt-receptors from the human lung Patent: WO 9946376-A 1 16-SEP-1999;
BASF AG (DE); KROEGER BURKHARD (DE)
Location/Qualifiers
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                                                                                                                                  Direct Submission
Submitted (21-DEC-1999) WP26A-1000, Merck Research Sumneytown Pike, West Point, PA 19403, USA Location/Qualifiers
                                                                                                                                                                                                                                                          Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
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                                                                  /cell
435.
/protein_id="AAF33685.1"
/db_xref="GI:6969261"
/translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
                                                                                       /chromosome="20"
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                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                               /product="M68C"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-09-936-024-1 (1-271) AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg GCCCAGTGCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCCACGACG GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGAGGGGAGCGGCTGGTGC ArgSerValArgGluArgPheLeuProValHis 271 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu CCCCACCGCAACTGCACGGCCCTGGGCCCTGAATGTGCCAGGCTCTTCCTCCCAT TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC CTGCTGGTGCGGCTGCAGGCGCGTGCGCGTGGCCAGGATGCCCGGGCTGGAG 6.79e-64 1491.00 100.00% 100.00% 100.00% 9 x AF217793 (1-1428)Length:
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Frediction of the coding sequences of unidentified human genes.

XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

DNA Res. 6 (3), 197-205 (1999)
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ORCQACWQRHLQASRMCPACHTASRKQSVMQVFWPEDFHKDHEGAAGGARPVAAVPGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:5689512:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="brain"
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                                            AB029011 4945 bp mRNA linear
Homo sapiens mRNA for KIAA1088 protein, partial cds.
AB029011
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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Search completed: January 6, 2003, 12:52:56

Job time : 2909 secs

Page 13

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_numan:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebra
14: sp_unclass:
15: sp_rurclass:
16: sp_aarcheap
17: sp_archeap
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sp_organelle:*
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sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ഗ	4.	w	2		Result No.
260	267.5	268.5	268.5	268.5	270.5	275	275	275	287	313.5	327	333.5	395	486.5	499.5	Score
17.4	17.9	18.0	18.0	18.0	18.1	18.4	18.4	18.4	19.2	21.0	21.9	22.4	26.5	32.6	33.5	Query Match L
348	349	349	349	349	349	348	348	348	651	433	482	459	302	285	285	Length
12	12	12	12	12	12	12	12	12	13	11	11	11	3	<u>1</u> 3	13	DB
057112	057099	057291	057102	057101	057100	057277	057108	057103	Q98SM6	Q91ZM6	088734	Q62327	Q9PUS0	984060	Q90W71	Ħ
057112 variola vir	057099 monkeypox v	057291 monkeypox v	057102 monkeypox v	057101 monkeypox v	O57100 monkeypox v	057277 monkeypox v	O57108 monkeypox v	O57103 monkeypox v	Q98sm6 gallus gall	Q91zm6 rattus norv	O88734 mus musculu	Q62327 mus musculu	Q9pus0 salvelinus	Q90ys6 oncorhynchu	Q90w71 oncorhynchu	Description

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200	202	203.5	219.5	227	230.5	244	245.5	248.5	249.5	251	252	253.5	253.5	253.5	254.5	254.5	257.5	257.5	257.5	257.5	258.5	259	260	260	260	260	260	260
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ALIGNMENTS

Ş	р Q	Que Mat	SQ	DR DR	DR DR	무	DR.	P 7	RA	RC	RP	Z S	8	88	3 6	멾	D.	3 5	AC	ij	RESULT Q90W71
62 CNVLCGEREBEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121	2 AETFTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61	Query Match 33.5%; Score 499.5; DB 13; Length 285; Best Local Similarity 37.1%; Pred. No. 5e-36; Matches 99; Conservative 41; Mismatches 116; Indels 11; Gaps 4;	Receptor. SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1. PROSITE; PS50050; TNFR_NGFR_2; 1.	Ptam; PF00020; TNFR c6; 3. PROSITE; PS01186; EGF_2; UNKNOWN_1.	InterPro; IPR001368; INFR_c6.	•	"Screening a rainbow trout (Oncornynchus mykiss) cDNA library."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.	Pleguezuelos O., Secombes C.J.;	TISSUE-HEAD KIDNEY;	SEQUENCE FROM N.A.	NCBI_TaxID=8022;	gii; Salmoniformes; Salm	Actinopteryqii: Neopteryqii: Teleostei: Euteleostei:	Oncornynchus mykiss (Rainbow trout) (Saimo gairdneri).	otor 3 protein.	01-JUN-2002 (TremBirel. 21, Last annotation update)			Q90W71 PRELIMINARY; PRT; 285 AA.	년 1 71

Euteleostomi;

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MEDLINE=20111091; PubMed=10642582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Murine tumour necrosis factor receptor 2 protein (Fragment)
                                                                                                       Decoy TNF receptor.
Salvelinus fontinalis (Brook trout) (Brook char).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelec Actinopterygii, Neopterygii; Teleostei; Biteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 7.7e-27; 44; Mismatches 101;
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Pred. No. 7.7e-27;
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     302
                                                        Created)
     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.5%;
34.3%;
                                                     01-MAY-2000 (TrEMBLrel. 13,
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFRSF1B.
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     셤
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                                                        QPCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
                                                                                                                                                               182 CERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
                                                                                                                                                                                              biu L., Fujiki K., Dixon B., Sundick R.S.;
Liu L., Fujiki K., Dixon B., Sundick R.S.;
Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
"Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
fragments containing AU-rich elements.";
Submitted (JUL-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AF401631; AAK91758.1;
InterPro; IPR001561; EGF-like.
InterPro; IPR001563; TNFR.c6.
Pfam; PF00020; TNFR.c6; 3.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oncornynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                          146 EPCPVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVYCSACTNG--SRTHEGEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
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rches 118;
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36.3%; Pred. No. 6.9e
tive 41; Mismatches
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PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
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                                                                                                                                                                                                                                                                             242 ALLVRLLQALRVARMPGLERSVRERFL 268
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                                                                                                                                                                                                                                                                                                                               256 -FAIQMRDILNTDŘLLHĽRTKVNKWFL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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SEQUENCE
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Best Local :
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O88734;
O1-NOV-1998 (Tr
O1-NOV-1998 (Tr
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P80 TNF-alpha r
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VARIANT
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VARIANT
EMBL; Y14619; CAA74969.1; JOINED. EMBL; Y14620; CAA74969.1; JOINED. EMBL; Y14621; CAA74969.1; JOINED. EMBL; Y14622; CAA74969.1; JOINED.
                                                                             MEDLINE=98414512; PubMed=9740674;
Hurle B., Segade F., Rodriguez R., Ramos S.S.
"The Mouse Tumor Necrosis Factor Receptor 2
and Characterization of the two Transcripts.
Genomics 52:79-98(1998).
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X76401; CAA53981.1; -. HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm. Genome 5:726-727(1994).
                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Powell E.E., Wicker L.S., Peter "Allelic variation of the type
                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                     TNFR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95178848; PubMed=7873884;
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STRAIN=NOD;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- ald
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93
268
345
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                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
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                                                                                                                                                                                                                                                                                           (Mouse)
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 333.5; 1
Pred. No. 3e-2:
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                              Ramos S.S., Lazo
                                                                                                                                                                                                                                                                                                                                                                                                                                          482
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                                                                                                                    Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110; Indels
                                                                                                                           Genomic
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                                                                                                                                              P.S.;
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                                                                                                                             Structure
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                                                                               Query Match
Best Local S
Matches 59
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Best Local S
Matches 82
                                                                                                                                                                    Receptor.
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SEQUENCE
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SMART; SM00208; TNFR; 4.

PROSITE; PS00652; TNFR NGFR 1;

PROSITE; PS50050; TNFR NGFR 2;
                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91ZM6 PRELIMINARY; PRT; 433 AA.
Q91ZM6; Q12M6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tumor necrosis factor receptor type II (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AF420214; AAL16021.1; -. InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                        Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., "TMF-receptors p60 and p80 are constitutively expressed by capillary endothelial cells and participate in TMF-alpha tr through the blood-brain barrier.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Y14623;
; Y14679;
; P19438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SI-----GLIMLGIVNCFILVQRKKKPSCLQRDAKVPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLVCAQCPPGTFVQRPCRR-----DSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGER
QMCCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQVETHNC
                                  RLVCAQCEPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLGAQDGALLVRLLQAL----RVARMPGLERSVRERFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTRSQPLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEECERAVIDEVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAPGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEEARACHATHNRACRCRTGFF----AHAGF----CLEHASCPPGAGVIAPGTPSQNTQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMCCAKCPPGQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTD
                                                                                                                                                                                                                                                      PF00020; TNFR_C6; 4.
TE; PS00652; TNFR_NGFR_1;
TE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
                                                                               Similarity 35.:
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 29.3
82; Conservative
                                                                                                                                                                    1
433
433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA74969.1; JOINED CAA74969.1; JOINED
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45723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; l
Rodentia; Sciurognathi; Muridae;
                                                                                                    21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.9%;
                                                                                                                                                                         WW.
                                                                                    29;
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                                                                             Score 313.5;
Pred. No. 1.6e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 327;
Pred. No. 1.
                                                                                                                                                                                                                                                             UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F6C15046B48FF83C
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                                                                                                                                                                         75736D835E72CA4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GSTPIIEQSTKGGISLPIGLIVGVT
                                                                               1.6e-19;
ches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
.2e-20;
                                                                                                                             DВ
                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 482;
                                                                                    Indels
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                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi; ; Murinae; Rat
                                                                                                                             433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                        rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bickel U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                      brain
                                                                                  Gaps
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91
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93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 PCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ZAIRE-1970;
Loparev V.N., Parsons J.M., Esposito J.J.;
"DNA sequence analysis as a criterion for allocation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
Local Similarity 33.1%; Pred. No. 3e-16;
les 59; Conservative 29; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 275; DB 12; Length 3 33.1%; Pred. No. 3e-16; ive 29; Mismatches 82; Indels
                                                                                                                Loparev V.N., Parsons J.M., Esposito J.J.; "DNA sequence analysis as a criterion for allocation of
                                                                                                                                                                           orthopoxviruses to a particular species.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; UB/847; AAB94364.1; -.
HSSP; O14763; 100G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       orthopoxviruses to a particular species.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88142; AAB94367.1; -.
HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 AA; 38184 MW; 34A5E668B27907B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA; 38212 MW; E555979057DEC91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor receptor II homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                        InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMATT; SM00208; TNFR; 2.
PROSITE; PS00052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR01168; TNFR c6.
Pfam; PF00020; TNFR c6; 2.
SMART; SM00208; TNFR, c6.
PROSITE; PS00652; TNFR NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                    SEQUENCE FROM N.A. STRAIN=ZAIRE-1979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10244;
NCBI_TaxID=10244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkeypox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162
                            HATHNRACRCRTGFFA----HAG---FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 DRATNQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 BEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCOPCPPGTFS 130
                                                              92 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkeypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
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Best Local Similarity 33.5%; Pred. No. 5.2e-17;
Matches 54; Conservative 27; Mismatches 80; Indels
                                                                                                                                                                                 152 SDTTSSTDVCRPHRICSILA---IPGNASTDAVCASES--PTPSAVP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Bridgham J.T., Johnson A.L.;

"Expression of DR6 in the ovary ";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;
                                                                                                                                               SASSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2002 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 ASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA.
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PROSITE; PS00652; TNFR NGFR 1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
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01-OCT-2001 (TrEMBLrel. 18,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus galīus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Death receptor 6
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Length 348;

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RESULT 10
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ID 05727
AC 05727
AC 05727
DT 01-JU
DT 01
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Best Local S
Matches 59
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01-JUN-1998
01-JUN-2002
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057277;
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EMBL; U87841; AAB94358.1; -..
EMBL; AF380138; AAL40648.1; -..
EMBL; AF380138; AAL40460.1; -..
HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001368; TNFR_c6. Pfam; PF00020; TNFR_c6; 2. SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TNFR NGFR 1; PROSITE; PS50050; TNFR NGFR 2; SEQUENCE 348 AA; 38212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V., Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A., Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21592287; PubMed=11734207;
Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss
Sandakhchiev L.S.;
"Human monkeypox and smallpox viruses: genomic comparison.";
FEBS Lett. 509:66-70(2001).
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STRAIN-ZAIRE-1996 /96-17, AN
Loparev V.N., Parsons J.M.,
Submitted (JAN-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkeypox virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ZAIRE-96-I-16;
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     152
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                                                                                                                                                                                                                                            RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE
                                                                                                                                                     RESEARACHATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                              KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS
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                                                   PCPPGTFSASSSSSSQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE
                                                                                                       NOVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS
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                                                                                                                                                                                                                                                                                                                                              Similarity
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(TTEMBLrel. 21, Last annotation update)
sis factor receptor II homolog (J2R) (J2L).
OR J2L.
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EMBL/GenBank/DDBJ databases.
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Pred.
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54019521556C2D8F CRC64;
                                                                                                                                                                                                                                                                                                                   Mismatches
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. No. 3e-16;
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RESULT 12
O5710
ID O5710
AC O5710
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT Tumor
GN CRMB.
OS WORK
OC Virus
OC Orthoc
OX NCBI.
RN (I)
RP SEQUE
RC STRAI
RA LOBAR
RT Orthc
RM EMBL.
DR HSSP;
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Best Local
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O57100;
Loparev V.N., Parsons J.M., Esposito J.J.; "DNA sequence analysis as a criterion for allocation of orthopoxviruses to a particular species."; Submitted (AN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; U87845; AAB94362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Tumor necrosis factor receptor II homolog.
                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                           SEQUENCE FROM N.A. STRAIN=ZAIRE-1977;
                                                                                                                             Viruses; dsDN/
Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                orthopoxviruses to a particular species.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monkeypox virus
                                                                                                             NCBI_TaxID=10244;
                                                                                                                                                     Monkeypox virus
                                                                                                                                                                              Tumor necrosis
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STRAIN=NIGERIA-1971;
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39; Conservative
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                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                              factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.1%; Score 270.5; 32.6%; Pred. No. 7.

    06, Created)
    06, Last sequence update)
    21, Last annotation updat
receptor II homolog.

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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DF6C280D478F2422 CRC64;
                                                                                                                                         stage;
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                                                                                                                                         Poxviridae;
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                                                                                                                                         Chordopoxvirinae;
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152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Poxyiridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, U87942; AAB94369.1; --
EMBL; U87942; AAB94365.1; --
EMBL; U87994; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94368.1; --
HSSP; O14763; IDDG.
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PROSITE; PS50050; TNFR NGFR 2; 2.
SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tumor necrosis factor receptor II homolog.
                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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NCBI_TaxID=10244;
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                                                                                                                                                                                                        DB 12; Length 349;
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STRAIN=BENIN-1978;
Loparev V.N., Parsons J.M., Esposito J.J.;
Loparev V.N., Parsons J. M., Esposito J.J.;
UNA sequence analysis as a criterion for allocation of the orthopoxylruses to a particular species.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   Query Match 18.0%; Score 268.5; DB 12; Length Best Local Similarity 32.6%; Pred. No. 1.1e-15; Matches 59; Conservative 29; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Indels
                                                                                                                                Receptor.
SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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HSSP, O14763; 1D0G.
InterPro; IPR001368; TWFR.c6.
Fram, PF00020; TWFR.c6; 2.
SMART; SM00208; TWFR, 2.
PROSITE; PS00052; TWFR NGFR.1; 2.
PROSITE; PS00050; TWFR NGFR.1; 2.
Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
PRART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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nes 59; Conservative
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NCBI_TaxID=10244;
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Search completed: January 6, 2003, 11:20:08 Job time : 75 secs
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STRAIN=SIERRA LEONE-1970;

Loparev V.N., Parsons J.M., Esposito J.J.;

"DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

REMBL; U87843; AAB94360.1; -.

REMBL; U87843; AAB94360.1; -.

REMBL; U87843; AAB94360.1; -.

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REMBL; DR
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Command line parameters:

-MODEL-frame, D2n.model -DEV=xlh
-Q-/Ggn2 1/USPTO spool/US09936024/runat_06012003_111607_12141/app_query.fasta_1.455
-DB=EST -QFWT=fastap -SUFFIX=D2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-Human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM-ext -HEABSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09936024 @CGN 1 1 1349 @runst_06012003 111607 12141 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMĀP -LĀRĞEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENT

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	BI821789	RESULT 1
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1118)</pre>	human. Homo sapiens	EST.	BI821789.1 GI:15933339	mRNA sequence. BI821789	603035863F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176910 5',	BI821789 1118 bp mRNA linear EST 04-OCT-2001		

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US-09-936-024-1 (1-271) x BQ687526 (1-863)
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/organism="Homo sapiens"
/db_xref="tcaxon:9606"
/clone="InMaGE:5176910"
/clone="InMaGE:5176910"
/clone="Organ: pooled brain, lung, testis; Vector:
/lab.host="DH108"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age for site 2: 2-7; and
male lung, age 27; and l male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
      Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1440 row: n column: 15
High quality sequence stop: 758.
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 863)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2394 row. c column: 12
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                                                                      540 AAGGCGGGCCGCGGGCCTTGCAGCTGAAGCTGCGTCGGCGCGCTCACGGAGCTCCTGGG
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

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/db xref="taxon:9606"
/clone="IMAGE:3894794"
/clone=lib="NIH_MGC_69"
/clone=lib="NIH_MGC_69"
/tissue_type="large_cell_carcinoma, undifferentiated"
/tissue_type="large_cell_carcinoma, undifferentiated"
/tab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
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Query Match: 71.36* Indels: 0 DB: 14 Gaps: 0 US-09-936-024-1 (1-271) x BM767535 (1-572) 0 40 ThrCysGlyProCysProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCys 59 QY 40 ThrCysGlyProCysProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCys 59 Db 2 AcGTGTGGCCGTGTCCACCGCGCACTACACGCAGTTCTCTGGAACTACTCTGGAACGAGCCTGC 61 QY 60 ArgTyrCysAsnValleuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThr 79 79 Db 62 CGCTACTGCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy 100 HisAlaSerCysProProGlyAlaGlyVall1eAlaProGlyThrProSerGlnAsnThr 119 182 CACGCATCGTCTCCACCTGGTGCCGGGTGATTGCCCCGGGCACCCCCAGCCAG	OY 160 HisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla 179 Db 362 CATGACACGTGTGCACCAGCTGCACCAGGACTACCAGGACT 421 OY 180 GluGluCysGluArgAlaValIleAspPheValAlaPheGluAspIleSerIleLySarg 199 Db 422 GAGGACTGTGACGTGCTCATCGACTTCCAGGACTACCAGGAGGT 421 OY 200 LeuGluArgLeuLeuGluAlaLeuGluAlaProGluGlyTrGGTTCCATCAAGAGG 481 OY 200 LeuGluArgLeuCluAlalaProGluGlyTrGGTTCCATCAAGAGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuGluAlaProGluGlyTrGGTTCCATCAAGAGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuCluArg 229 Db 542 GGCCGCGGCTTGCAGCTCTGAGGCCCTGGAGGGTTCCAAGAGGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuGluArg 229 Db 542 GGCCGCGGCCTTGCAGCTCTGAGGCTCTGAGGGTTCCAAGGGG 541 OY 220 GlyArgAlaAlaLeuGluAlaProGluArg 229 Db 542 GGCCGCGGCCTTGCAGCTCGAGGCCCTGGAGGGTTCCAAGGGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuGluArg 229 Db 542 GGCCGCGCGCCTTGCAGCTCGAGGCCCTGGAGGGTTCCAAGGGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuCysLarg 229 Db 542 GGCCGCGCGCCTTGCAGCTCGAGGCCCTGGAGGGTTCCAAGGGG 541 OY 220 GlyArgAlaAlaLeuGluAlaLeuCysLarg 229 Db 542 GGCCGCGCGCCTTGCAGGCCTCGAGGCCTGGAGGGTTCCAAGGGG 541 OY 220 GlyArgAlaAlaLeuGluArg 229 DCUS BGG79499 LCCUS BGG79499 LCC	Email: cgapbersemail.nin.gov Tissue Procurement: James Cleaver, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMl0610 row: k column: 04 High quality sequence stop: 762. FEATURES Location/Qualifiers
BM767535 ION K-EST005 IRNA seq ON BM767535 S BT/ Numan. ISM Homo sap Eukaryot. TSM Homo sap Eukaryot. CE 1 (base Kim, N. S. Kim, N. S. Z1C Fron. AL Unpublisl	COMMINITY CONGECT: ALM CONGENT Research Institute of Bioscience & Biotechnology Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 3 row: E column: 03 High quality sequence stop: 572. Location/Qualifiers 1. 572 Lorganism="Homo sapiens" /organism="Homo sapiens" /db xref="taxon:9606"	/clone=1518NU5s2.3.203. /clone=1b="S18NU5s2.3.203." /clone=1b="S18NU5s2.3.203." /clone=1b="S18NU5s2.3.203." /cell_LYpe="Lymphoblast-like" /cell_Lype="Months John John	Inbraries were constructed by transformation of the remaining DNA into competent cells E. coli ToploF' with electroporation method." BASE COUNT 90 a 213 c 174 g 95 t ORIGIN Alignment Scores: 4.43e-80 Length: 572 Score: 1664.00 Matches: 190 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0

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/clone lib="NCI CGAP Skn4"
/clone lib="NCI CGAP Skn4"
/tissue_type="squamous cell carcinoma"
/lab host="DH10B (Tl phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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Location/Qualifiers
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5', mRNA Sequence.
BM480117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1203)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5491790"
/clone=lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Technologies.
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MAGE:5491790
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/urganism="Homo sapiens"

/db_xref="taxon:9606"
/clone="ur=bol-ajc-j-12-0-ur"
/clone="ur=bol-ajc-j-12-0-ur"
/clone="ur=bol-ajc-j-12-0-ur"
/clone="ur=bol-ajc-j-12-0-ur"
/clone="ur=bol-"bol-"bol-"bol-"bol-"bol-"bullobe"
/dev stage="fetal"
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/lab_bost="blidb (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pec (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-ED1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector: The oligonuclecitde used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT) B tail. The sequence tag for this library is
CGGTATACC: This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
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TAG_TISSUE=human fetal eye
TAG_SEQ=CGCGTATACC"
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Best Local Similarity:
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Program for Rat Gene Discovery and Mapping
University of Lowa
University of Lowa
University of Lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 9266
Fax: 319 335 9565
Email: msoarces@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Forward
POLYA=Yes:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 728)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln
                                                                                          CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
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Best Local Similarity:
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                                                                                                                                                                                           TGCCACGCCAC-CACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT
                                                     TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 679)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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High quality sequence stop: 672.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP/Gazdar
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:3891908"
/clone=1ib="NIH MGC 69"
/clone_1ib="NIH MGC 69"
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/lab host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
/site_3: Sall; Cloned unidirectionally. Onstructed by Life
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5', mRNA sequence.
BF339551
BF339551.1 GI:11286006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                          129
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                                                                                                                    /clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 299 c 301 g 145 t
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/db_xref="taxon:9606"
/clone="IMAGE:4186995"
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University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewinGuiuc.edu Email: h-lewinGuiuc.edu Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length. FOR PRIMERS	/ Jeak-Tenale" / Jab_host="Hemale" / Jab_host="DH10B" / Jace="Organ: placenta, Vector: pT7T3Pac, Site_1: EcoRI; / Jace="Organ: placenta, Vector: pT7T3Pac, Site_1: EcoRI; Site_2: NotI: The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. " ORIGIN ORIGIN	Alignment Scores: 2.08e-63 Length: 554 Pred. No.: 866.00 Matches: 147 Score: 147 Percent Similarity: 91.62\$ Conservative: 6 Best Local Similarity: 88.02\$ Mismatches: 14 Query Match: 58.08\$ Indels: 0 DB: 0.05-09-936-024-1 (1-271) x AW464298 (1-554)	Qy 2 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAla 21	Qy 42 GlyProCysBroProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyr 61 Db 172 GGTGCGTGCCGCGCCCCATACACACATTTTGGAACTACCTGGAGCGCGCGC
ery Matc : -09-936- 1 185 21 245	Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120 bb 485 GCATCGTGCCCACCTGGTGCCGGGGTTGCCCCGGGGCCCCCCAGCAGAACACGCGG 514 Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGeTGGlnCysGln 140 Db 545 TGCCAGCGTGCCCCCCAGGCAACTTCTCAGCCAGCAGCTCCAGCTCCAGCTGCCAG 604 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160	Db 605 CCCCACCAACTGCACGCCTCGGCCTCAATGTGCCAGGCTCTTCCTCCCAT 663 Qy 161 ASPTHALEUCYS-THISERCYSTHIG19PHEPROLEUSERTHIARGVA1PROG19A1aG1 180 Db 664 GACACCCTGTGGCACCAGCTGCATTCCCCCTCAGCACAGGGTACAGGGTTGA 720 Qy 180 uGlu-CysGluArgAlaVa1I1eAspPheValAlaPheG1nAspI1eSerI1e1ysArg1 200 181	Qy 200 euGlnargLeuLeuGlnalaLeuGlualaProGluGJyTrpGJyProThrProArgAlaG 220 Db 781 GCGCGGTGTGGGCCTTAGGCCCGGAGGTGG 810 Qy 220 lyArgAla 222 Db 811 GGTCCGCC 818	RESULT 10 AW464298 LOCUS BP230015A20G11 Soares normalized bovine placenta Bos taurus CDNA CLOCUS BP230015A20G11 Soares normalized bovine placenta Bos taurus CDNA CLOCUS CLOCUS AW464298 ACCESSION AW464298.1 G1:7034466 EST. COW. SOURCE COW. SOURCE COW. BOX taurus BOX taurus BOX taurus BUKATYOLA; Matazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; BOX taurus AUTHORS JOURNAL COURNAL COURNAL CONMENT W. M. Keck Center for Comparative and Functional Genomics

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ThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSer 133
                                                                    CTG---TTTCTGCTGGAGCACGCATCGTGTCCACCTGT-GCCGGCGTGATTGCCCCGGGC
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Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michae
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 692)
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Location/Qualifiers
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/db xref="taxon:9606"
/clone="IMAGE:2583534"
/clone_lib="NCI_CGAP_Co21"
/tissue_type="moderately differentiated adenocarcinoma"
/tissue_type="moderately differentiated adenocarcinoma"
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B1838357
B1838357.1 GI
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                    High quality sequence stop:
Location/Qualifiers
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National Institutes of Health, Mammalian
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1 (bases 1 to 588)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                      /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5222545"
/clone lib="NIH MGC 120"
/lab_host="DH10B"
(EcoRV site is destroyed upon cloning). Average size 1.5 kb, insert size range 1-2.5 kb. Librar normalized and enriched for full-length clones constructed by C. Gruber (Invitrogen). Research
                                                                           'note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site1: Not1; Site2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
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605 bp mRNA linear EST 04-MAR-2002 K-EST0049137 SISNU5s2 Homo sapiens cDNA clone SISNU5s2-4-D01 5', BM767088
                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='InhaGB:2752231"
/clone=lib="NCI GAPp_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/note="Organ: lung, Vector: pCWV-SPORT6, Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
a 177 c 199 g 102 t 2 others
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarhini, Hominidae, Homo.
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Mismatches:
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www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Fechnologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 600)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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     this is a NIH MGC Library." t 1 others
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Conservative:
Mismatches:
Indels:
  tracking code 025. Note: t
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Best Local Similarity:
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TITLE
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Kim, N.S.,
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Genome Research Institute of Bioscience & Biotechnology
Korea Research Vinsenng-qu, Daejeon 305-333, South Korea
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Contact: Kim YS
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21C Frontier Korean EST Project 2001
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Plate: 4 row: D column: 01
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Tel: +82-42-860-4470
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1, N.S., Hahn, Y., Oh

K.J., Cheong, J.E.,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription with single stranded RNA by in vitro transcription
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/cell_type="Lymphoblast-like"
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/db_xref="taxon:9606"
/clone="S1SNU5s2-4-D01"
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Kim, N.S., Hahn, Y., Oh
Oh, K.J., Cheong, J.E.,
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21C Frontier Korean EST Project 2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: 5 row: B column: 04
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/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
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/clone="S1SNU5s2-5-B04"
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line="SNU-5"
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, Daejeon 305-333, South Korea
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obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF, by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 primer and N(dT)14 as 3 primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA IND-RNA hybrids by centrifuge, the subtracted cDNA remaining DNA into competent cells E. coli ToplOF' with
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Search completed: January 6, 2003, 12:04:15 Job time : 1972 secs

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Title:
Perfect score:
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Listing first 45 summaries
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PIR_73:*
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Gapop 10.0 , Gapext 0.5
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1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match 1	Length	80	ID	Description
r	340.5	22.8	461	_		
2	333.5	22.4	459	N	u	murine t
w	332.5	22.3	474	N	B38634	
4	299.5	•	435	N	w	tumor necrosis
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89	260		349	N	D36858	970
9	234.5		325	2	B43692	T2 protein - rabb
10	215.5	•	277	N	I37552	0 homolog
11	211.5		271	ν	S12783	
12	211	14.	277	N	A60771	Š
13	210.5	14.	326	_	GQVZML	T2 protein - myxom
14	203	13.	305	N	A46476	cel1
15	194.5	13.	272	N	I48700	
16	185	12.	256	N	B32393	T-cell antigen 4-1
17	182	12.2	595	Ν	A42086	
18	174	11.	255	N	I38426	
19	171.5	11.	416	μ	JN0006	nerve growth fact
20	168	11.	425	<u>س</u>	A26431	
21	158	10.	427	Н	GQHUN	nerve growth fact
22	155.5	10.	327	Ν	A46484	apoptosis-mediat
23	148.5	10.	1574	Ν	T13954	MEGF6 protein -
24	148	9.	250	۲	A49053	CD27 antigen precu
25	147.5	9.	5376	N	T42215	1
26	146.5	9.8	260	_	A46517	CD27 antigen p
27	145	9.	335	N	A40036	apoptosis-mediatin
28	143	9.	1620	N	T27283	hypothetical prote
ر و	100	۵	,			

ALIGNMENTS

A; Rocessou: A3000 A; Status: preciminary A; Molecule type: mRNA A; Residues: 116-140, 'p',142-195, 'R',197-362,'T',364-461 <hel> A; Residues: 116-140, 'p',142-195, 'R',197-362,'T',364-461 <hel> A; Residues: 126-140, 'p',142-195, 'R',197-362,'T', 364-461 <hel> A; Cross-references: GB: M35857; NID:g339751; PIDN. AAA63362.1; PID:g339752 A; Cross-references: Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990 A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MUID:91056048; PMID:2173696 A; Recession: A23666 A; Accession: A23666 A; Molecule type: protein A; Residues: 23-40;65-69;136-141;300-306 <loe></loe></hel></hel></hel>	ry Ny DEM DEM GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649 GB:S63368; NCBIP:63371) tracted from NCBI backbone (NCBIN:63368, NCBIP:63371) tracted from N.A.; Fischer, W.H.; Chang, D.; Ringold, Ci. U.S.A. 87, 6151-6155, 1990 ary DNA cloning of a receptor for tumor necrosis factor A36007; MUID:90349572; PMID:2166946	PIDN:AAA36755.1; p] m, H.W.; Gentz, R.; ular, but distinct	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-461 <smi> A; Cross-references: GB:M32315; NID:gl89185; PIDN:AAA59929.1; PID:gl89186 A; Cross-references: GB:M32315; NID:gl89185; P.E.; King, M.W.; Hale, K.K.; Squ R; Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squ Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990 A; Title: A second tumor necrosis factor receptor gene product can shed a naturally A; Reference number: A36475; MUID:91045991; PMID:2172983 A; Accession: A36475</smi>	A35356 tumor necrosis factor receptor 2 precursor [validated] - human tumor necrosis factor receptor; TNF receptor type 2 N,Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2 C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 08-Dec-2000 C;Accession: A35356, A36475; A48416; A36007; A23666; B85010; I38094 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular A;Reference number: A35356; MUID:90260639; PMID:2160731 A;Accession: A35356
ockhaus, M. ct tumor neci	G.M. and demonstrat	D:g339758 Brockhaus, M.; intracellular,	K.K.; Squires,	; Dower, S.K. ellular and \

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A, Residues: 1-459 <RES>
A, Cross-references: BMBL:X76401, NID:9433830, PIDN:CAA53981.1, PID:9433831
C. Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                 Query Match
Best Local Similarity
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A,Molecule type: mRNA
A,Residues: 1-474 <LEW>
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Matches 81; Conserv
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A; Residues: 1-22 <KIS>
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   R,Engelmann, H.; Novick, D.; Wallach, D.

Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215; PMID:2153136
                                                                                                                                                                                                                                 R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region
A;Reference number: 138094; MUID:95121934; PMID:7821811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: GDB:125914; OMIM:191191
A/A position: 1D36.2-1D36.2
A/Introns: 26/3
A/Introns: 26/3
A/Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <AGINGS-
F;18-119/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
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R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
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C,Species: Mus musculus (house mouse)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 VCTSTS--PTRSMAPGAVHLPQPV----STRSQHTQPTPEPSTAPSTSFLLPMGPSP 249
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
                                                                                                                                                       :Status: preliminary
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                                                                                                                        A; Accession: B35010
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A; Molecule type: mRNA

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tumor necrosis factor receptor type 2 precursor - mouse (5gpecies: Mus musculus (house mouse) (2gpecies: Mus musculus (house mouse) (2bate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999 (2gccssion: B38634; A40224; S54816 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E A;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; MUID:91187885; PMID:1849278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen's Molecular cloning and expression of the type 1 and type 2 murine receptors for A; Reference number: A40254; MUID:91246168; PMID:1645445
A; Accession: A40254
A; Molecule type: mRNA
A; Residues: 1-74 <GOO-A; Cross-references: GB: M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R; Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
A; Residues: Cheracterization of the promoter region of the murine p75-TNF receptor.
A; Reference number: S54816
A; Accession: S54816
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                                                                                                                                                                                                                                                                                                                                                              97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 SASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP----RAGRAALQLKLRRRLTELLGAQD 240
                                                                                                                                                                                                                                                                                                              77 HATHNRACRCRIGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
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                                                                                                                                                                                                               37 QMCCAKCPPGQYVKHFCNKTSDTVCADCBASMYTQVWNQFRTCLSCSSSCSTDQVETRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 PLD----QSPPGPSQTPSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----
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                                                                           43; Mismatches 110;
   Score 333.5; DB 2
Pred. No. 6.3e-18;
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22.4%;
29.7%;
                                                                               81; Conservative
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C;Accession: I54182
C;Accession: I54182
R;Beens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
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death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine \
A;Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                        RESULT
JC7705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Crose-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision
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A;Map position: 12p13.3-12p13.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptor 2-related protein - human
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                     LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLVRLLQAL----RVARMPGLERSVRERFLP 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREBEARAC
                                                                                                                                                                                                                                   LAVLLPLAFFILLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG
                                                                                                                                                                                                                                                                         ERAVIDEVAFQDIS----
                                                                                                                                                                                                                                                                                                          PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPENSGTMLM
                                                                                                                                                                                                                                                                                                                                                PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC
                                                                                                                                                                                                                                                                                                                                                                                                                     EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 32.0
74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.1%; Score 299.5; DB 2; 32.0%; Pred. No. 2.2e-15; tive 27; Mismatches 101;
                                                                                                                                                                                                                                                                       ----IKRLORLLOALEAPEGWGPTPRAG 220
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C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin, R;Massung, R.F.; Bsposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin, Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus (A;Reference number: Z20488; MUID:94088747; PMID:8264798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-21/Domain: signal sequence #status predicted <SIG>F;52-196/Domain: extracellular cysteine-rich, ligand-binding F;33-350/Domain: transmembrane #status predicted <TMM>F;410-475/Domain: death domain #status predicted <DED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Comment: This receptor, a member of the tumor necrosis factor receptor tresia, activates a cell death and/or survival signaling cascade. C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T28623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:gA;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-348 < MAS>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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Best Local (
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206
                                                                                                                                              118 NTQCQPCPPGTFSASSSSSSSQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 ASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFP
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TSE
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                                                                                                 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL
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                                                                                                                                                                                                                                                     VLCGEREEEARACHATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                                                                                                                                                                                                                                                                                                    PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN
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33.5%; Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 260; DB 2; 32.2%; Pred. No. 1.7e-12; tive 26; Mismatches 90
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Gaps

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Length 349;

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88 GRCNSNOVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146
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                                                                                                                                                          receptor repeat homology
A;Experimental source: strain India-1967, ssp. major C;Genetics:
A;Gene: GR.
C;Superfamily: myxoma virus T2 protein; NGF receptor F;32-66/Domain: NGF receptor repeat homology «NGF» F;68-109/Domain: NGF receptor repeat homology «NG2» F;110-151/Domain: NGF receptor repeat homology «NG3»
                                                                                                                                                                                                                                                                                                                                                                                          17.4%; Score 260; DB 2;
32.2%; Pred. No. 1.7e-12;
tive 26; Mismatches 90
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Best Local Similarity
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Matches 52; Conserv
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OX40 homolog - human
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C;Species: variola virus
C;Species: variola virus
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 23-Mar-2001
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Accession: Dis658
A;Accession: Dis658
A;Accession: Dis658
A;Accession: Sin India-1967, ssp. major, isolate Ind3
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
A;Cross-reference number: S4686
A;Betrence number: S4688
A;Reture: preliminary
A;Molecule type: DNA
A;Reture: preliminary
A;Molecule 
                                                                                                                                                                              R.;Abchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A.;Abescription: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Reference number: A72150
A;Reference preliminary
A;Status: preliminary
A;Residues: 1-349 < SHC>
A;Residues: 1-349 < SHC>
A;Residues: 1-349 < SHC>
A;Residues: 1-349 < CHC>
A;Residues: 1-349 < CHC>
A;Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
A;Cross-references: strain Garcia-1966
C;Genetics:
A;Genetics:
A;Gen
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A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
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                                            C;Spēcies: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 VLCGEREEEARACHATHNRACRCRIGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
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variola minor virus (strain Garcia-1966)
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A,Residues: 31-168 <SHC>
A,Cross-references: EMBL:X69198
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RESULT 9
1843692
12 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
N;Tology 160, 20-30, 1987
A;Title: Tumoriganic poxviruses: genomic organization and DNA sequence of the telomeric A;Reference number: A43692; MUID:87321103; PMID:2820128
A;Accession: B43692
A;Accession: B43692
A;Residues: 1-325 <UPT>
B;G105/Domain: NGF receptor repeat homology <NG3>
F;106-147/Domain: NGF receptor repeat homology <NG3>
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: 137552
R;Latza, U; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fons:
Bur. J. Immunol. 24, 677-683, 1994
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A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment A;Reference number: I37552; MUID:94170844; PMID:7510240 A;Accession: I37552
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A; Residues: 1-271 < MAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S12783; S08036
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    RESULT 12
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Best Local
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Best Local
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                                                                LGVDCVPCPPGHF - - SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC
                                                                                                                                                                                                                            TYP----SGHK-CCRECOPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCN
                                                                                                                                                                                                                                                                     TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRSG--SERKQLCTATQDTVCRCRAG-----TQPLDSYKPG------VDCAP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN
                                                                                                      --- QCQPCPPGTFSASSSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPPGHF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPSNDR-----CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN 88
                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%;
                                                                                                                                                                                                                                                                                                                              14.2%; Score 211.5; DB 2; 31.5%; Pred. No. 6.4e-09;
                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 215.5; DB 2
Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104; Indels
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                               ----PGTQPRQDSSHK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 277;
                                                                                                                                                                                                                                                                                                                                                    Length 271;
                                                              163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g57831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g472958
                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positive T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                     63
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Query Match
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A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1;
A;Cross-references: GB:M95181; protein; NGF receptor repeat homology
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth fac.
A;Reference number: S04460; MUID:89356608; PMID:2475341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T2 protein - myxoma virus (strain Lausanne)
c;Species: myxoma virus
c;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
C;Accession: A40566
C;Accession: A40566
C;Accession: A40566
C;Accession: A40566
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane F;1-20/Domain: signal sequence #status predicted <SIG> F;21-20/Domain: B-cell activation protein CD40 #status experimental <MAT> F;21-193/Domain: extracellular #status predicted <EXT> F;194-215/Domain: transmembrane #status predicted <TMM> F;194-215/Domain: intracellular #status predicted <CYT> F;195-277/Domain: intracellular #status predicted <CYT> F;195-277/Domain: difference #status predicted <CYT> F;195-277/Domain: diffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;BraesCh-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 20q12-20q13.2
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 21-50 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAFEKCHPWTSCETKDLVVQQAGTNKTDVVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ET--DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HATHNRACRCRTGFFAHA---GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTS
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Pred. No. 7.1e-09;
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                                     (covalent) #status predicted
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                                                                                                                                                                                                                                                                                           PID: g332310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis
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14.1%; Score 210.5;

DB 1;

Length 326;

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rch completed: January
time : 39 secs
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                                                                                                                                                                                                                                                                                                                  Matches
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 HATHNRACRCRIGFFA---HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ATHNRACRCRIGFFA-----HAGFCLEHASCPPGAGVIAPGTPSONTOCOPCPPGTFSA 131
                                                                                               38 LCCTSCPPGSYASKLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESOSCD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEARAC 76
                                  18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEARACH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                       - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
           Indels
                                                                                                                                                                                                                     cell-associated surface molecule CD40, long splice form
           80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.6%; Score 203; DB 2;
Best Local Similarity 31.1%; Pred. No. 3.1e-08;
                                                                                                                                                          AVSSTETCTSSFNYISVEFNL ----YPVNDTSCTTTAG 190
                                                                                                                                   SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
 No. 9.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches
           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLFEKCYPWISCEDKNLEVLOKGISQINVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
 Pred.
30.4%;
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            Conservative
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 Best Local Similarity
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               Matches
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6, 2003, 11:21:00

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R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell in A;Reference number: 148700; MJID:94044750; PMID:8228223
                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
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A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: 1-14, 'G', 16-272 <RE2>
A;Residues: 1-14, 'G', 16-272 <RE2>
C;Genetics: EMBL:XB5214; NID:g732818; PIDN:CAAS9476.1; PID:g732819
C;Genetics: A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 194.5; DB 2; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 --- QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 LGVDĊVPCPPGHF--SPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                      A,Accession: 148700
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                      A; Residues: 1-272 <RES>
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